

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 10:59:57 ; Search time 39 Seconds  
(without alignments)  
61.625 Million cell updates/sec

Title: US-09-549-642-20  
Perfect score: 138  
Sequence: 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match %	Length	ID	Description
1	101	73.2	271	2 S29239	chymotrypsin (EC 3
2	94	68.1	265	2 T10495	chymotrypsin (EC 3
3	91	65.9	31	2 S61558	chymotrypsin Pml -
4	89	64.5	226	1 KCUF	brachyurin (EC 3.4
5	80	58.0	31	2 S18356	chymotrypsin (EC 3
6	74	53.6	309	2 B49878	coagulation factor
7	71	51.4	20	2 A56900	chymotrypsin I (EC
8	69	50.0	271	2 A25528	pancreatic elastase
9	69	50.0	460	2 B61545	plasmin (EC 3.4.21
10	69	50.0	1524	2 T30337	polypeptide - Afri
11	68	49.3	25	2 A23698	trypsin (EC 3.4.2
12	67	48.6	23	2 P00036	serine proteinase
13	67	48.6	244	2 S72219	chymotrypsin B - A
14	67	48.6	268	2 S68826	pancreatic elastase
15	67	48.6	268	2 S68825	pancreatic elastase
16	66	47.8	271	1 ELRT2	pancreatic elastase
17	65	47.1	262	1 A31372	granzyme A (EC 3.4
18	64	46.4	269	2 B26823	pancreatic elastase
19	63	45.7	20	2 A34817	collagenolytic pro
20	63	45.7	269	2 A26823	pancreatic elastase
21	63	45.7	273	2 A47246	trypsin (EC 3.4.2
22	63	45.7	274	2 C45754	trypsin (EC 3.4.2
23	63	45.7	275	2 C35863	trypsin (EC 3.4.2
24	63	45.7	812	1 PLMS	plasmin (EC 3.4.21
25	63	45.7	812	1 PLBO	apolipoprotein(a)
26	63	45.7	1420	2 A32869	apolipoprotein(a)
27	63	45.7	4548	1 S00657	alkaline trypsin-1
28	62	44.9	24	2 P00657	hypothetical prote
29	62	44.9	331	2 T27906	

30 62 44.9 810 1 PLHU plasmin (EC 3.4.21  
31 61 44.2 810 2 B30848 plasmin (EC 3.4.21  
32 61 44.2 1035 1 A43090 enteropeptidase (E  
33 60 43.5 270 2 S56160 mast cell tryptase  
34 60 43.5 790 1 PLPG plasmin (EC 3.4.21  
35 59 42.8 260 2 I56559 neuropsin - mouse  
36 59 42.8 261 2 A29586 tissue kallikrein  
37 59 42.8 261 2 S40162 cathepsin G (EC 3.  
38 59 42.8 263 2 S47537 chymotrypsin (EC 3  
39 59 42.8 269 2 C26823 pancreatic elastase  
40 59 42.8 810 2 I46260 plasmin (EC 3.4.21  
41 58 42.0 262 1 KQHU tissue kallikrein  
42 58 42.0 269 2 B32410 mastocytoma protei  
43 57 41.3 25 2 A35545 t-kininogenase (EC  
44 57 41.3 31 2 B33257 pancreatic elastase  
45 57 41.3 245 1 KYBOA chymotrypsin (EC 3

ALIGNMENTS

RESULT 1  
S29239  
chymotrypsin (EC 3.4.21.1) 1 precursor - penaeid shrimp (Penaeus vanamei)  
C:Species: Penaeus vanamei  
C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 22-Jun-1999  
C:Accession: S29239; S22075  
R:Sellos, D.; van Wormhoudt, A.  
FEBS Lett. 309, 219-224, 1992  
A:Title: Molecular cloning of a cDNA that encodes a serine protease with chymotryptic  
A:Reference-number: S29239; MUID:92387359; PMID:1516690  
A:Accession: S29239  
A:Molecule type: mRNA  
A:Residues: 1-271 <SEL>  
A:Cross-references: EMBL:X66415; NID:g10088; PIDN:CAA47046.1; PID:g10089  
A:Note: the authors did not translate the codon for residue 1  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; protein digestion; serine proteinase  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-271/Product: chymotrypsin 1 #status predicted <SIG>  
F:46-263/Domain: trypsin homology <TRY>  
F:86,132,223/Active site: His, Asp, Ser #status predicted

Query Match 73.2% Score 101; DB 2; Length 271;  
Best Local Similarity 72.0%; Pred. No. 7.4e-08;  
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25  
Db 46 IVGGVEATPHSWPQAALFIDDMYF 70  
|||||  
|||||

RESULT 2  
T10495  
chymotrypsin (EC 3.4.21.1) BII - penaeid shrimp (Penaeus vanamei) (fragment)  
C:Species: Penaeus vanamei  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Jun-2000  
C:Accession: T10495  
R:Sellos, D.Y.; van Wormhoudt, A.  
submitted to the EMBL Data Library, January 1997  
A:Description: Polymorphism of chymotrypsin gene sequences in the shrimp.  
A:Reference number: Z17057  
A:Accession: T10495  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-265 <SEL>  
A:Cross-references: EMBL:X10665  
C:Genetics:  
A:Note: Chymotrypsin B  
A:Note: Intron positions not resolved (incomplete sequence)  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; protein digestion; serine proteinase

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Db          1  IVGGVEAVPNSPHQAALFIDDMYF 25
||||| 1 1:::1 1|||||||
RESULT 5
SI8356
Chymotrypsin (EC 3.4.21.1) Pm2 - penaeid shrimp (Penaeus monodon) (fragment)
C:Species: Penaeus monodon
C:Date: 22-Nov-1993 #sequence_revision 01-Mar-1996 #text_change 01-Nov-1996
C:Accession: SI8356
R:Tsay, I.H.; Lu, P.J.; Chuang, J.L.
Biochim. Biophys. Acta 1080, 59-67, 1991
A:Title: The midgut chymotrypsins of shrimps (Penaeus monodon, Penaeus japonicus and
A:Reference number: SI8356; MUID:92031652; PMID:1657178
A:Accession: SI8356
A:Molecule type: protein
A:Residues: 1-31 <TSA>
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; protein digestion; serine proteinase
Query Match      58.0%; Score 80; DB 2; Length 31;
Best Local Similarity 60.0%; Pred. No. 1.le-05;
Matches 15; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY      1  IVGGXEVTPHAYPMOVGLFIDDMYF 25
||||| 1 1:::1 1|||||||
Db      1  IVGGVEAVPCVWPYQAAALFIDDMYF 25
||||| 1 1:::1 1|||||||
RESULT 6
B49878
Coagulation factor G beta chain precursor - horseshoe crab (Tachyplesus tridentatus)
C:Species: Tachyplesus tridentatus
C:Date: 30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change 20-Jun-2000
C:Accession: B49878
R:Seiki, N.; Muta, T.; Oda, T.; Iwaki, D.; Kuma, K.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 269, 1370-1374, 1994
A:Title: Horseshoe crab (1,3)-beta-D-glucan-sensitive coagulation factor G. A serine
A:Reference number: A49878; MUID:94117453; PMID:8288603
A:Accession: B49878
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-309 <SEX>
A:CROSS-References: GB:DL6623; NID:g459415; PIDN:BAA04045.1; PID:g459416
C:Superfamily: trypsin; trypsin homology
C:Keywords: hemolymph coagulation; heterodimer; serine proteinase; zymogen
E:47-287/Domain: trypsin homology <TRY>
Query Match      53.6%; Score 74; DB 2; Length 309;
Best Local Similarity 57.9%; Pred. No. 0.0012;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY      1  IVGGXEVTPHAYPMOVGLF 19
||||| 1 1:::1 1|||||||
Db      47  IIGGGIATPHSPWPMVGVIF 65
||||| 1 1:::1 1|||||||
RESULT 7
A56900
Chymotrypsin I (EC 3.4.21.-) - penaeid shrimp (Penaeus vanamei) (fragment)
C:Species: Penaeus vanamei
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 20-Jun-2000
C:Accession: A56900
R:Van Wormhoudt, A.; Le Chevalier, P.; Sellios, D.
Comp. Biochem. Physiol. B 103, 675-680, 1992
A:Title: Purification, biochemical characterization and N-terminal sequence of a serin
apoda).
A:Reference number: A56900; MUID:93092601; PMID:1458841
A:Accession: A56900
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <VAN>
A:Note: sequence extracted from NCBI backbone (NCBIP.120229).

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A:Description: Purification and characterization of a novel serine proteinase from bovin  
A:Reference number: PU0036  
A:Accession: PU0036  
A:Molecule type: protein  
A:Residues: 1-23 <TSU>  
A:Experimental source: pancreas  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine proteinase

Query Match 48.6%; Score 67; DB 2; Length 23;  
Best Local Similarity 50.0%; Pred. No. 0.00075;  
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPMQVGL 18  
:||||: |||:||||: |  
Db 1 VVGGEAIPHSWPQVLSL 18

## RESULT 13

A:Description: trypsin B - Atlantic cod (fragments)  
A:Reference number: Gadus morhua (Atlantic cod)  
A:Accession: S72219  
C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Aug-1998  
R:Leth-Larsen, R.; Asgeirsson, B.; Thorolfsson, M.; Norregaard-Madsen, M.; Hojrup, P.  
Biochim. Biophys. Acta 1297, 49-56, 1996  
A:Title: Structure of chymotrypsin variant B from Atlantic cod, Gadus morhua.  
A:Reference number: S72219; MUID:96439045; PMID:8841380  
A:Accession: S72219  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14;15-244 <LET>  
C:Superfamily: trypsin; trypsin homology  
F:15-237/Domain: trypsin homology <TRY>

Query Match 48.6%; Score 67; DB 2; Length 244;  
Best Local Similarity 61.1%; Pred. No. 0.011;  
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPMQVGL 18  
||| ||| |||:||||| |  
Db 15 IVNGEAVPHSWPQVSL 32

## RESULT 14

A:Description: pancreatic elastase (EC 3.4.21.36) isoform 2 precursor - human  
A:Reference number: caldecrin isoform 2  
A:Accession: S68826  
C:Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998  
R:Tomomura, A.; Akiyama, M.; Itoh, H.; Yoshino, I.; Tomomura, M.; Nishii, Y.; Noikura, T.  
FEBS Lett. 386, 26-28, 1996  
A:Title: Molecular cloning and expression of human caldecrin.  
A:Reference number: S68825; MUID:96221265; PMID:8635596  
A:Accession: S68826  
A:Molecule type: mRNA  
A:Residues: 1-268 <TOM>  
A:Experimental source: pancreas  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; pancreas; serine proteinase; zymogen  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-29/Domain: propeptide #status predicted <PRO>  
F:30-268/Product: pancreatic elastase isoform 2 #status predicted <MAT>  
F:30-262/Domain: trypsin homology <TRY>

Query Match 48.6%; Score 67; DB 2; Length 268;  
Best Local Similarity 50.0%; Pred. No. 0.012;  
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPMQVGL 18  
:||||: |||:||||| |  
Db 30 VVGGEAIPHSWPQVLSL 47

## RESULT 15

A:Description: pancreatic elastase (EC 3.4.21.36) isoform 1 precursor - human  
A:Reference number: caldecrin isoform 1  
A:Accession: S68825  
C:Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 28-May-1999  
R:Tomomura, A.; Akiyama, M.; Itoh, H.; Yoshino, I.; Tomomura, M.; Nishii, Y.; Noikura, T.  
FEBS Lett. 386, 26-28, 1996  
A:Title: Molecular cloning and expression of human caldecrin.  
A:Reference number: S68825; MUID:96221265; PMID:8635596  
A:Accession: S68825  
A:Molecule type: mRNA  
A:Residues: 1-268 <TOM>  
A:Cross-references: GB:S82198; NID:g1839466; PIDN:AAB47104.1; PID:g1839467  
A:Experimental source: pancreas  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; pancreas; serine proteinase; zymogen  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-29/Domain: propeptide #status predicted <PRO>  
F:30-268/Product: pancreatic elastase isoform 1 #status predicted <MAT>  
F:30-262/Domain: trypsin homology <TRY>

Query Match 48.6%; Score 67; DB 2; Length 268;  
Best Local Similarity 50.0%; Pred. No. 0.012;  
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY -1 IVGGXEVTPHAYPMQVGL 18  
:||||: |||:||||| |  
Db 30 VVGGEAIPHSWPQVLSL 47

Search completed: May 30, 2003, 11:04:55  
Job time : 40 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	136	98.6	25	5	US-09-303-375A-1	Sequence 1, Appli
2	136	98.6	25	5	US-09-303-375A-2	Sequence 2, Appli
3	136	98.6	25	5	US-09-549-642-1	Sequence 1, Appli
4	136	98.6	25	5	US-09-549-642-2	Sequence 2, Appli
5	136	98.6	25	5	US-09-549-642-20	Sequence 20, Appli
6	136	98.6	300	5	US-09-644-022A-1	Sequence 1, Appli
7	101	73.2	25	5	US-09-644-022A-2	Sequence 2, Appli
8	101	73.2	25	5	US-09-303-375A-3	Sequence 3, Appli
9	101	73.2	25	5	US-09-549-642-3	Sequence 3, Appli
10	91	65.9	25	5	US-09-644-022A-6	Sequence 6, Appli
11	91	65.9	25	5	US-09-303-375A-7	Sequence 7, Appli
12	91	65.9	25	5	US-09-549-642-7	Sequence 7, Appli
13	89	64.5	25	5	US-09-644-022A-7	Sequence 7, Appli
14	89	64.5	25	5	US-09-303-375A-8	Sequence 8, Appli
15	89	64.5	25	5	US-09-549-642-8	Sequence 8, Appli
16	80	58.0	25	5	US-09-644-022A-5	Sequence 5, Appli
17	80	58.0	25	5	US-09-303-375A-6	Sequence 6, Appli
18	80	58.0	25	5	US-09-549-642-6	Sequence 6, Appli
19	75.5	54.7	287	1	PCM-US02-10780-130	Sequence 130, App
20	75.5	54.7	287	6	US-10-114-270-130	Sequence 130, App
21	75.5	54.7	602	7	US-60-452-680-23138	Sequence 23138, A
22	75.5	54.7	922	1	PCM-US02-10366-52	Sequence 52, Appli
23	75.5	54.7	932	6	US-10-363-937-6	Sequence 6, Appli
24	75.5	54.7	986	1	PCM-US02-10366-50	Sequence 50, Appli
25	70	50.7	273	6	US-10-219-051B-8824	Sequence 8824, A
26	70	50.7	273	6	US-10-219-051B-13255	Sequence 13255, A

; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Euphausia superba  
US-09-303-375A-2

Query Match 98.6%; Score 136; DB 5; Length 25;  
Best Local Similarity 96.0%; Pred. No. 1.4e-13;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
||||| ||||||| ||||||| ||||||| |||||||  
Db 1 IVGGMEVTPHAYPWQVGLFIDDMYF 25

RESULT 3  
US-09-549-642-1  
; Sequence 1, Application US/09549642  
; GENERAL INFORMATION:  
; APPLICANT: Phairson Medical, Inc.  
; APPLICANT: de Faire, Johan  
; APPLICANT: Franklin, Richard L.  
; APPLICANT: Kay, John  
; APPLICANT: Lindblom, Ragnvald  
; TITLE OF INVENTION: Removing Dental Plaque with Krill  
; FILE REFERENCE: 314572-101F  
; CURRENT APPLICATION NUMBER: US/09/549,642  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 09/303,375  
; PRIOR FILING DATE: 2000-04-30  
; PRIOR APPLICATION NUMBER: 08/600,273  
; PRIOR FILING DATE: 1996-02-08  
; PRIOR APPLICATION NUMBER: 08/486,820  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/385,540  
; PRIOR FILING DATE: 1995-02-08  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Euphausia superba  
US-09-549-642-1

Query Match 98.6%; Score 136; DB 5; Length 25;  
Best Local Similarity 96.0%; Pred. No. 1.4e-13;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
||||| ||||||| ||||||| ||||||| |||||||  
Db 1 IVGGMEVTPHAYPWQVGLFIDDMYF 25

RESULT 4  
US-09-549-642-2  
; Sequence 2, Application US/09549642  
; GENERAL INFORMATION:  
; APPLICANT: Phairson Medical, Inc.  
; APPLICANT: de Faire, Johan  
; APPLICANT: Franklin, Richard L.  
; APPLICANT: Kay, John  
; APPLICANT: Lindblom, Ragnvald  
; TITLE OF INVENTION: Removing Dental Plaque with Krill  
; FILE REFERENCE: 314572-101F  
; CURRENT APPLICATION NUMBER: US/09/549,642  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 09/303,375  
; PRIOR FILING DATE: 2000-04-30  
; PRIOR APPLICATION NUMBER: 08/600,273

; PRIOR FILING DATE: 1996-02-08  
; PRIOR APPLICATION NUMBER: 08/486,820  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/385,540  
; PRIOR FILING DATE: 1995-02-08  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Euphausia superba  
US-09-549-642-2

Query Match 98.6%; Score 136; DB 5; Length 25;  
Best Local Similarity 96.0%; Pred. No. 1.4e-13;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
||||| ||||||| ||||||| ||||||| |||||||  
Db 1 IVGGMEVTPHAYPWQVGLFIDDMYF 25

RESULT 5  
US-09-549-642-20  
; Sequence 20, Application US/09549642  
; GENERAL INFORMATION:  
; APPLICANT: Phairson Medical, Inc.  
; APPLICANT: de Faire, Johan  
; APPLICANT: Franklin, Richard L.  
; APPLICANT: Kay, John  
; APPLICANT: Lindblom, Ragnvald  
; TITLE OF INVENTION: Removing Dental Plaque with Krill  
; FILE REFERENCE: 314572-101F  
; CURRENT APPLICATION NUMBER: US/09/549,642  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 09/303,375  
; PRIOR FILING DATE: 2000-04-30  
; PRIOR APPLICATION NUMBER: 08/600,273  
; PRIOR FILING DATE: 1996-02-08  
; PRIOR APPLICATION NUMBER: 08/486,820  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/385,540  
; PRIOR FILING DATE: 1995-02-08  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Euphausia superba  
; NAME/KEY: VARIANT  
; LOCATION: (1)-(25)  
; OTHER INFORMATION: Xaa - Any Amino Acid  
US-09-549-642-20

Query Match 98.6%; Score 136; DB 5; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.4e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
||||| ||||||| ||||||| ||||||| |||||||  
Db 1 IVGGXVTPHAYPWQVGLFIDDMYF 25

RESULT 6  
US-09-644-022A-1  
; Sequence 1, Application US/09644022A  
; GENERAL INFORMATION:  
; APPLICANT: Franklin, Richard L.  
; APPLICANT: Cowling, Didier S.P.  
; APPLICANT: Hubbel, Jeffrey A.  
; APPLICANT: van de Wetering, Petra

;; TITLE OF INVENTION: Treatment of Trauma  
;; FILE REFERENCE: 314572-103B  
;; CURRENT APPLICATION NUMBER: US/09/644,022A  
;; CURRENT FILING DATE: 2000-08-23  
;; NUMBER OF SEQ ID NOS: 17  
;; SOFTWARE: FastSEQ for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 300  
;; TYPE: PRP  
;; ORGANISM: Panaeus vanamei  
US-09-644-022A-1

Query Match 98.6%; Score 136; DB 5; Length 300;  
Best Local Similarity 96.0%; Pred. No. 1.7e-12;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25  
Db 64 IVGGMEVTPHAYPMQVGLFIDDMYF 88

US-09-644-022A-2

;; Sequence 2, Application US/09644022A  
;; GENERAL INFORMATION:  
;; APPLICANT: Franklin, Richard L.  
;; APPLICANT: Cowling, Didier S.P.  
;; APPLICANT: Hubbel, Jeffrey A.  
;; APPLICANT: van de Metering, Petra  
;; TITLE OF INVENTION: Treatment of Trauma  
;; FILE REFERENCE: 314572-103B  
;; CURRENT APPLICATION NUMBER: US/09/644,022A  
;; CURRENT FILING DATE: 2000-08-23  
;; NUMBER OF SEQ ID NOS: 17  
;; SOFTWARE: FastSEQ for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 25  
;; TYPE: PRP  
;; ORGANISM: Panaeus vanamei  
US-09-644-022A-2

Query Match 73.2%; Score 101; DB 5; Length 25;  
Best Local Similarity 72.0%; Pred. No. 2.9e-08;  
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQHAALFIDDMYF 25

RESULT 8

US-09-303-375A-3  
;; Sequence 3, Application US/09303375A  
;; GENERAL INFORMATION:  
;; APPLICANT: Johan R. de Faire  
;; APPLICANT: Richard L. Franklin  
;; APPLICANT: John Kay  
;; APPLICANT: Ragnvald Lindblom  
;; TITLE OF INVENTION: Multifunctional Enzyme  
;; FILE REFERENCE: 314572-101E  
;; CURRENT APPLICATION NUMBER: US/09/303,375A  
;; CURRENT FILING DATE: 1999-04-30  
;; PRIOR APPLICATION NUMBER: US 08/486,820  
;; PRIOR FILING DATE: 1995-06-07  
;; PRIOR APPLICATION NUMBER: US 08/385,540  
;; PRIOR FILING DATE: 1995-02-08  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: FastSEQ for Windows Version 4.0  
;; SEQ ID NO 3  
;; LENGTH: 25  
;; TYPE: PRP  
;; ORGANISM: Panaeus vanamei  
US-09-303-375A-3

Query Match 73.2%; Score 101; DB 5; Length 25;  
Best Local Similarity 72.0%; Pred. No. 2.9e-08;  
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQHAALFIDDMYF 25

RESULT 9

US-09-549-642-3  
;; Sequence 3, Application US/09549642  
;; GENERAL INFORMATION:  
;; APPLICANT: Phairson Medical, Inc.  
;; APPLICANT: de Faire, Johan  
;; APPLICANT: Franklin, Richard L.  
;; APPLICANT: Kay, John  
;; APPLICANT: Lindblom, Ragnvald  
;; TITLE OF INVENTION: Removing Dental Plaque with Krill  
;; FILE REFERENCE: 314572-101F  
;; CURRENT APPLICATION NUMBER: US/09/549,642  
;; CURRENT FILING DATE: 2000-04-14  
;; PRIOR APPLICATION NUMBER: 09/303,375  
;; PRIOR FILING DATE: 2000-04-30  
;; PRIOR APPLICATION NUMBER: 08/600,273  
;; PRIOR FILING DATE: 1996-02-08  
;; PRIOR APPLICATION NUMBER: 08/486,820  
;; PRIOR FILING DATE: 1995-06-07  
;; PRIOR APPLICATION NUMBER: 08/385,540  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: FastSEQ for Windows Version 4.0  
;; SEQ ID NO 3  
;; LENGTH: 25  
;; TYPE: PRP  
;; ORGANISM: Panaeus vanamei  
US-09-549-642-3

Query Match 73.2%; Score 101; DB 5; Length 25;  
Best Local Similarity 72.0%; Pred. No. 2.9e-08;  
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQHAALFIDDMYF 25

RESULT 10

US-09-644-022A-6  
;; Sequence 6, Application US/09644022A  
;; GENERAL INFORMATION:  
;; APPLICANT: Franklin, Richard L.  
;; APPLICANT: Cowling, Didier S.P.  
;; APPLICANT: Hubbel, Jeffrey A.  
;; APPLICANT: van de Metering, Petra  
;; TITLE OF INVENTION: Treatment of Trauma  
;; FILE REFERENCE: 314572-103B  
;; CURRENT APPLICATION NUMBER: US/09/644,022A  
;; CURRENT FILING DATE: 2000-08-23  
;; NUMBER OF SEQ ID NOS: 17  
;; SOFTWARE: FastSEQ for Windows Version 4.0  
;; SEQ ID NO 6  
;; LENGTH: 25  
;; TYPE: PRP  
;; ORGANISM: Panaeus monodon chymotryptic  
US-09-644-022A-6

Query Match 65.9%; Score 91; DB 5; Length 25;  
Best Local Similarity 64.0%; Pred. No. 9.7e-07;  
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 IVGGXVTPHAYPQVQGLFIDDMYF 25  
||||| |:::| | | | |  
Db 1 IVGGVEAVPHSWPYQAALFIDDMYF 25

RESULT 11  
US-09-303-375A-7  
; Sequence 7, Application US/09303375A  
; GENERAL INFORMATION:  
; APPLICANT: Johan R. de Faire  
; APPLICANT: Richard L. Franklin  
; APPLICANT: John Kay  
; APPLICANT: Ragnvald Lindblom  
; TITLE OF INVENTION: Multifunctional Enzyme  
; FILE REFERENCE: 314572-101E  
; CURRENT APPLICATION NUMBER: US/09/303,375A  
; CURRENT FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: US 08/486,820  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: US 08/385,540  
; PRIOR FILING DATE: 1995-02-08  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Panaeus monodon  
US-09-303-375A-7

Query Match 65.9%; Score 91; DB 5; Length 25;  
Best Local Similarity 64.0%; Pred. No. 9.7e-07;  
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 IVGGXVTPHAYPQVQGLFIDDMYF 25  
||||| |:::| | | | |  
Db 1 IVGGVEAVPHSWPYQAALFIDDMYF 25

RESULT 12  
US-09-549-642-7  
; Sequence 7, Application US/09549642  
; GENERAL INFORMATION:  
; APPLICANT: Phairson Medical, Inc.  
; APPLICANT: de Faire, Johan  
; APPLICANT: Franklin, Richard L.  
; APPLICANT: Kay, John  
; APPLICANT: Lindblom, Ragnvald  
; TITLE OF INVENTION: Removing Dental Plaque with Krill  
; FILE REFERENCE: 314572-101F  
; CURRENT APPLICATION NUMBER: US/09/549,642  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 09/303,375  
; PRIOR FILING DATE: 2000-04-30  
; PRIOR APPLICATION NUMBER: 08/600,273  
; PRIOR FILING DATE: 1996-02-08  
; PRIOR APPLICATION NUMBER: 08/486,820  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/385,540  
; PRIOR FILING DATE: 1995-02-08  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Panaeus monodon  
US-09-549-642-7

Query Match 65.9%; Score 91; DB 5; Length 25;  
Best Local Similarity 64.0%; Pred. No. 9.7e-07;  
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 IVGGXVTPHAYPQVQGLFIDDMYF 25

Db 1 IVGGVEAVPHSWPYQAALFIDDMYF 25  
||||| |:::| | | | |

RESULT 13  
US-09-644-022A-7  
; Sequence 7, Application US/09644022A  
; GENERAL INFORMATION:  
; APPLICANT: Franklin, Richard L.  
; APPLICANT: Cowling, Didier S.P.  
; APPLICANT: Hubbel, Jeffrey A.  
; APPLICANT: van de Wetering, Petra  
; TITLE OF INVENTION: Treatment of Trauma  
; FILE REFERENCE: 314572-103B  
; CURRENT APPLICATION NUMBER: US/09/644,022A  
; CURRENT FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Uca pugnator enzyme  
US-09-644-022A-7

Query Match 64.5%; Score 89; DB 5; Length 25;  
Best Local Similarity 64.0%; Pred. No. 2e-06;  
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 IVGGXVTPHAYPQVQGLFIDDMYF 25  
||||| |:::| | | | |  
Db 1 IVGGVEAVPHSWPYQAALFIDDMYF 25

RESULT 14  
US-09-303-375A-8  
; Sequence 8, Application US/09303375A  
; GENERAL INFORMATION:  
; APPLICANT: Johan R. de Faire  
; APPLICANT: Richard L. Franklin  
; APPLICANT: John Kay  
; APPLICANT: Ragnvald Lindblom  
; TITLE OF INVENTION: Multifunctional Enzyme  
; FILE REFERENCE: 314572-101E  
; CURRENT APPLICATION NUMBER: US/09/303,375A  
; CURRENT FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: US 08/486,820  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: US 08/385,540  
; PRIOR FILING DATE: 1995-02-08  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Uca pugnator  
US-09-303-375A-8

Query Match 64.5%; Score 89; DB 5; Length 25;  
Best Local Similarity 64.0%; Pred. No. 2e-06;  
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 IVGGXVTPHAYPQVQGLFIDDMYF 25  
||||| |:::| | | | |  
Db 1 IVGGVEAVPHSWPYQAALFIDDMYF 25

RESULT 15  
US-09-549-642-8  
; Sequence 8, Application US/09549642  
; GENERAL INFORMATION:  
; APPLICANT: Phairson Medical, Inc.  
; APPLICANT: de Faire, Johan  
; APPLICANT: Franklin, Richard L.



```

; APPLICANT: Kay, John
; APPLICANT: Lindblom, Ragnvald
; TITLE OF INVENTION: Removing Dental Plaque with Krill
; TITLE OF INVENTION: Enzymes
; FILE REFERENCE: 314572-101F
; CURRENT APPLICATION NUMBER: US/09/549,642
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 09/303,375
; PRIOR FILING DATE: 2000-04-30
; PRIOR APPLICATION NUMBER: 08/600,273
; PRIOR FILING DATE: 1996-02-08
; PRIOR APPLICATION NUMBER: 08/486,820
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/385,540
; PRIOR FILING DATE: 1995-02-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Uca pugilator
; 9-549-642-8

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Query Match      64.5%; Score 89; DB 5; Length 25;
Best Local Similarity 64.0%; Pred. NO. 2e-06;
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY      1 IVGGXEVTPHAYPMQVGLFIDDMYF 25
Db      1 IVGGVEAVPNSWPHQAALFIDDMYF 25

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Search completed: May 30, 2003, 11:12:20
Job time : 89 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 11:01:13 ; search time 26 Seconds  
(without alignments)  
28.291 Million cell updates/sec

Title: us-09-549-642-20

Perfect score: 138

Sequence: 1 IVGXEVTPHAYPMQVGLFIDDMYF 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A-COMB.pap.\*  
2: /cgn2\_6/ptodata/1/1aa/5B-COMB.pap.\*  
3: /cgn2\_6/ptodata/1/1aa/6A-COMB.pap.\*  
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5: /cgn2\_6/ptodata/1/1aa/PCTUS-COMB.pap.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	136	98.6	25	2	US-08-385-540A-1
2	136	98.6	25	2	US-08-385-540A-2
3	136	98.6	25	2	US-08-385-540A-17
4	136	98.6	25	2	US-08-600-273A-1
5	136	98.6	25	2	US-08-600-273A-2
6	136	98.6	25	2	US-08-600-273A-17
7	136	98.6	25	3	US-08-486-820-1
8	136	98.6	25	3	US-08-486-820-2
9	136	98.6	25	3	US-08-486-820-17
10	136	98.6	25	3	US-08-705-875A-19
11	136	98.6	25	4	US-09-220-731-1
12	136	98.6	25	4	US-09-220-731-2
13	136	98.6	25	4	US-09-220-731-20
14	136	98.6	178	3	US-08-705-875A-8
15	136	98.6	178	4	US-09-220-731-23
16	136	98.6	178	4	US-09-220-731-24
17	136	98.6	300	3	US-08-705-875A-4
18	136	98.6	300	3	US-08-705-875A-6
19	136	98.6	300	4	US-09-220-731-21
20	136	98.6	302	4	US-09-220-731-26
21	136	98.6	308	3	US-08-705-875A-10
22	123	89.1	23	4	US-09-220-731-19
23	101	73.2	25	2	US-08-385-540A-3
24	101	73.2	25	2	US-08-600-273A-3
25	101	73.2	25	3	US-08-486-820-3
26	101	73.2	25	4	US-09-220-731-3
27	96	69.6	211	4	US-09-220-731-25

Sequence 7, Appli  
Sequence 7, Appli  
Sequence 7, Appli  
Sequence 7, Appli  
Sequence 8, Appli  
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Sequence 4, Appli  
Sequence 5, Appli  
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Sequence 6, Appli  
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Sequence 4, Appli  
Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-08-385-540A-1  
; Sequence 1, Application US/08385540A  
; Patent No. 5945102  
; GENERAL INFORMATION:  
; APPLICANT: de Faire, Johan  
; TITLE OF INVENTION: Wound Care With Multifunctional  
; TITLE OF INVENTION: Enzyme  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dechert Price & Rhoads  
; STREET: 997 Lenox Drive, Building 3, Suite 210  
; CITY: Lawrenceville  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08543  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/385.540A  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/600.273  
; FILING DATE: 08-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bloom, Allen  
; REGISTRATION NUMBER: 29,135  
; REFERENCE/DOCKET NUMBER: 314572-101A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-520-3214  
; TELEFAX: 609-520-3259  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-385-540A-1

Query Match 98.6%; Score 136; DB 2; Length 25;  
Best Local Similarity 96.0%; Pred. No. 3.5e-15;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 IVGXEVTPHAYPMQVGLFIDDMYF 25  
|||||

Db 1 IVGGNEVTPHAYPWQVGLFIDDMYF 25

RESULT 2

US-08-385-540A-2

Sequence 2, Application US/08385540A

Patent No. 5945102

GENERAL INFORMATION:

APPLICANT: de Faire, Johan

TITLE OF INVENTION: Wound Care With Multifunctional

TITLE OF INVENTION: Enzyme

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price & Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/385,540A

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/600,273

FILING DATE: 08-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 314572-101A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-520-3214

TELEFAX: 609-520-3259

TELEX:

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-385-540A-17

Query Match 98.6%; Score 136; DB 2; Length 25;

Best Local Similarity 100.0%; Pred. No. 3.5e-15;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVGGNEVTPHAYPWQVGLFIDDMYF 25

Db 1 IVGGNEVTPHAYPWQVGLFIDDMYF 25

RESULT 4

US-08-600-273A-1

Sequence 1, Application US/08600273A

Patent No. 5958406

GENERAL INFORMATION:

APPLICANT: de Faire, Johan

APPLICANT: Franklin, Richard L.

APPLICANT: Kay, John

TITLE OF INVENTION: Acne Treatment With Multifunctional

TITLE OF INVENTION: Enzyme

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price & Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/600,273A

FILING DATE: 08-FEB-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/486,820

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/385,540

FILING DATE: 08-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 314572-101C

Qy 1 IVGGNEVTPHAYPWQVGLFIDDMYF 25

Db 1 IVGGNEVTPHAYPWQVGLFIDDMYF 25

RESULT 3

US-08-385-540A-17

Sequence 17, Application US/08385540A

Patent No. 5945102

GENERAL INFORMATION:

APPLICANT: de Faire, Johan

TITLE OF INVENTION: Wound Care With Multifunctional

TITLE OF INVENTION: Enzyme

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price & Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

COMPUTER READABLE FORM:

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-620-3214

TELEFAX: 609-620-3259

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-600-273A-1

Query Match 98.6%; Score 136; DB 2; Length 25;

Best Local Similarity 96.0%; Pred. No. 3.5e-15;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPQVGLFIDDMYF 25

Db 1 IVGGNEVTPHAYPQVGLFIDDMYF 25

BT 5

US-08-600-273A-2

Sequence 2, Application US/08600273A

Patent No. 5958406

GENERAL INFORMATION:

APPLICANT: de Faire, Johan

APPLICANT: Franklin, Richard L.

APPLICANT: Kay, John

TITLE OF INVENTION: Acne Treatment With Multifunctional

TITLE OF INVENTION: Enzyme

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price &amp; Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/600,273A

FILING DATE: 08-FEB-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/486,820

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/385,540

FILING DATE: 08-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 314572-101C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-620-3214

TELEFAX: 609-620-3259

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-600-273A-2

Query Match 98.6%; Score 136; DB 2; Length 25;

Best Local Similarity 96.0%; Pred. No. 3.5e-15;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPQVGLFIDDMYF 25

Db 1 IVGGNEVTPHAYPQVGLFIDDMYF 25

RESULT 6

US-08-600-273A-17

Sequence 17, Application US/08600273A

Patent No. 5958406

GENERAL INFORMATION:

APPLICANT: de Faire, Johan

APPLICANT: Franklin, Richard L.

APPLICANT: Kay, John

TITLE OF INVENTION: Acne Treatment With Multifunctional

TITLE OF INVENTION: Enzyme

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price &amp; Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/600,273A

FILING DATE: 08-FEB-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/486,820

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/385,540

FILING DATE: 08-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 314572-101C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-620-3214

TELEFAX: 609-620-3259

TELEX:

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-600-273A-17

Query Match 98.6%; Score 136; DB 2; Length 25;

Best Local Similarity 100.0%; Pred. No. 3.5e-15;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPQVGLFIDDMYF 25

Db 1 IVGGNEVTPHAYPQVGLFIDDMYF 25

RESULT 7

US-08-486-820-1

Sequence 1, Application US/08486820

Patent No. 6030612

GENERAL INFORMATION:

APPLICANT: de Faire, Johan

APPLICANT: Franklin, Richard L.

APPLICANT: Kay, John

TITLE OF INVENTION: Antimicrobial Uses Of Multifunctional



Query Match 98.6%; Score 136; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3.5e-15;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGXVTPHAYPWQVGLFIDDMYF 25

RESULT 10  
US-08-705-875A-19  
Sequence 19, Application US/08705875A  
Patent No. 6040155  
GENERAL INFORMATION:  
APPLICANT: Kay, John  
TITLE OF INVENTION: ENZYME AND DNA SEQUENCE ENCODING  
TITLE OF INVENTION: SAME  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dechert Price & Rhoads  
STREET: 997 Lenox Drive, Building 3, Suite 210  
CITY: Lawrenceville  
STATE: NJ  
COUNTRY: USA  
ZIP: 08543  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/705,875A  
FILING DATE: 28-AUG-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/768,318  
FILING DATE: 17-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bloom, Allen  
REGISTRATION NUMBER: 29,135  
REFERENCE/DOCKET NUMBER: 314572-102US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-520-3214  
TELEFAX: 609-520-3259  
TELEX:  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-705-875A-19

Query Match 98.6%; Score 136; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3.5e-15;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGXVTPHAYPWQVGLFIDDMYF 25

RESULT 11  
US-09-220-731-1  
Sequence 1, Application US/09220731A  
Patent No. 6232088  
GENERAL INFORMATION:  
APPLICANT: Phairson Medical, Inc.  
APPLICANT: Richard L. Franklin  
APPLICANT: Yves St. Pierre  
TITLE OF INVENTION: Treatment and Prevention of Immune

TITLE OF INVENTION: Rejection Reactions  
FILE REFERENCE: 314572-101D  
CURRENT APPLICATION NUMBER: US/09/220,731A  
CURRENT FILING DATE: 1998-12-24  
EARLIER APPLICATION NUMBER: PCT/SE93/00455  
EARLIER FILING DATE: 1993-05-21  
EARLIER APPLICATION NUMBER: 08/338,501  
EARLIER FILING DATE: 1994-11-22  
EARLIER APPLICATION NUMBER: 08/385,540  
EARLIER FILING DATE: 1995-02-08  
EARLIER APPLICATION NUMBER: 08/486,820  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/600,273  
EARLIER FILING DATE: 1996-02-08  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Euphasia superba  
US-09-220-731-1

Query Match 98.6%; Score 136; DB 4; Length 25;  
Best Local Similarity 96.0%; Pred. No. 3.5e-15;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGXVTPHAYPWQVGLFIDDMYF 25

RESULT 12  
US-09-220-731-2  
Sequence 2, Application US/09220731A  
Patent No. 6232088  
GENERAL INFORMATION:  
APPLICANT: Phairson Medical, Inc.  
APPLICANT: Richard L. Franklin  
APPLICANT: Yves St. Pierre  
TITLE OF INVENTION: Treatment and Prevention of Immune  
TITLE OF INVENTION: Rejection Reactions  
FILE REFERENCE: 314572-101D  
CURRENT APPLICATION NUMBER: US/09/220,731A  
CURRENT FILING DATE: 1998-12-24  
EARLIER APPLICATION NUMBER: PCT/SE93/00455  
EARLIER FILING DATE: 1993-05-21  
EARLIER APPLICATION NUMBER: 08/338,501  
EARLIER FILING DATE: 1994-11-22  
EARLIER APPLICATION NUMBER: 08/385,540  
EARLIER FILING DATE: 1995-02-08  
EARLIER APPLICATION NUMBER: 08/486,820  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/600,273  
EARLIER FILING DATE: 1996-02-08  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Euphasia superba  
US-09-220-731-2

Query Match 98.6%; Score 136; DB 4; Length 25;  
Best Local Similarity 96.0%; Pred. No. 3.5e-15;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGXVTPHAYPWQVGLFIDDMYF 25

RESULT 13  
US-09-220-731-20

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; Sequence 20, Application US/09220731A
; Patent No. 6232088
; GENERAL INFORMATION:
; APPLICANT: Phairson Medical, Inc.
; APPLICANT: Richard L. Franklin
; APPLICANT: Yves St. Pierre
; TITLE OF INVENTION: Treatment and Prevention of Immune
; REJECTION REACTIONS
; FILE REFERENCE: 314572-101D
; CURRENT APPLICATION NUMBER: US/09/220,731A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: PCT/SE93/00455
; EARLIER FILING DATE: 1993-05-21
; EARLIER APPLICATION NUMBER: 08/338,501
; EARLIER FILING DATE: 1994-11-22
; EARLIER APPLICATION NUMBER: 08/385,540
; EARLIER FILING DATE: 1995-02-08
; EARLIER APPLICATION NUMBER: 08/486,820
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/600,273
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Euphasia superba
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (5)...(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-220-731-20
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```
Query Match 98.6%; Score 136; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25
|||||
Db 1 IVGGXVTPHAYPMQVGLFIDDMYF 25
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RESULT 14
US-08-705-875A-8
; Sequence 8, Application US/08705875A
; Patent No. 6040155
; GENERAL INFORMATION:
; APPLICANT: Kay, John
; APPLICANT: Kille, Peter
; TITLE OF INVENTION: ENZYME AND DNA SEQUENCE ENCODING
; TITLE OF INVENTION: SAME
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,875A
; FILING DATE: 28-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/768,318
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
```

```
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 314572-102US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-705-875A-8
```

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Query Match 98.6%; Score 136; DB 3; Length 178;
Best Local Similarity 96.0%; Pred. No. 3.3e-14;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25
|||||
Db 72 IVGGXVTPHAYPMQVGLFIDDMYF 96
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RESULT 15
US-09-220-731-23
; Sequence 23, Application US/09220731A
; Patent No. 6232088
; GENERAL INFORMATION:
; APPLICANT: Phairson Medical, Inc.
; APPLICANT: Richard L. Franklin
; APPLICANT: Yves St. Pierre
; TITLE OF INVENTION: Treatment and Prevention of Immune
; REJECTION REACTIONS
; FILE REFERENCE: 314572-101D
; CURRENT APPLICATION NUMBER: US/09/220,731A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: PCT/SE93/00455
; EARLIER FILING DATE: 1993-05-21
; EARLIER APPLICATION NUMBER: 08/338,501
; EARLIER FILING DATE: 1994-11-22
; EARLIER APPLICATION NUMBER: 08/385,540
; EARLIER FILING DATE: 1995-02-08
; EARLIER APPLICATION NUMBER: 08/486,820
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/600,273
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Euphasia
US-09-220-731-23
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Query Match 98.6%; Score 136; DB 4; Length 178;
Best Local Similarity 96.0%; Pred. No. 3.3e-14;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25
|||||
Db 72 IVGGXVTPHAYPMQVGLFIDDMYF 96
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Search completed: May 30, 2003, 11:05:29
Job time : 27 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 11:04:17 ; Search time 45 Seconds  
(without alignments)  
56.235 Million cell updates/sec

Title: us-09-549-642-20

Perfect score: 138

Sequence: 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 10123694 residues

number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	136	98.6	300	9	US-09-938-269-1
2	101	73.2	25	9	US-09-938-269-2
3	91	65.9	25	9	US-09-938-269-6
4	89	64.5	25	9	US-09-938-269-7
5	80	58.0	25	9	US-09-938-269-5
6	75.5	54.7	970	10	US-09-888-615-101
7	70	50.7	272	9	US-10-117-323-37
8	69	50.0	271	9	US-10-117-323-39
9	68	49.3	20	9	US-09-938-269-3
10	67	48.6	252	9	US-10-117-323-38
11	66	47.8	229	9	US-09-898-837A-53
12	66	47.8	260	9	US-09-978-295A-395
13	66	47.8	260	9	US-09-978-697-395
14	66	47.8	260	9	US-09-978-192A-395
15	66	47.8	260	9	US-09-999-832A-395
16	66	47.8	260	9	US-09-978-189-395
17	66	47.8	260	9	US-10-028-072-396
18	66	47.8	260	9	US-10-121-049-396
19	66	47.8	260	9	US-10-123-032-396

20	66	47.8	260	9	US-10-140-470-396	Sequence 396, App
21	66	47.8	260	9	US-10-175-746-396	Sequence 396, App
22	66	47.8	260	9	US-10-176-918-396	Sequence 396, App
23	66	47.8	260	9	US-10-176-921-396	Sequence 396, App
24	66	47.8	260	9	US-10-137-865-396	Sequence 396, App
25	66	47.8	260	9	US-10-140-474-396	Sequence 396, App
26	66	47.8	260	9	US-10-142-431-396	Sequence 396, App
27	66	47.8	260	9	US-10-143-114-396	Sequence 396, App
28	66	47.8	260	9	US-10-140-002-396	Sequence 396, App
29	66	47.8	260	9	US-09-978-608A-395	Sequence 395, App
30	66	47.8	260	9	US-10-142-419-396	Sequence 396, App
31	66	47.8	260	9	US-09-978-191A-395	Sequence 395, App
32	66	47.8	260	9	US-09-978-403A-395	Sequence 395, App
33	66	47.8	260	9	US-09-978-564A-395	Sequence 395, App
34	66	47.8	260	9	US-09-978-585A-395	Sequence 395, App
35	66	47.8	260	9	US-10-017-081A-395	Sequence 395, App
36	66	47.8	260	9	US-10-123-262-396	Sequence 396, App
37	66	47.8	260	9	US-10-142-423-396	Sequence 396, App
38	66	47.8	260	9	US-09-978-824-395	Sequence 395, App
39	66	47.8	260	9	US-09-981-915A-395	Sequence 395, App
40	66	47.8	260	9	US-09-999-833A-395	Sequence 395, App
41	66	47.8	260	9	US-10-121-050-396	Sequence 396, App
42	66	47.8	260	9	US-10-141-755-396	Sequence 396, App
43	66	47.8	260	9	US-10-167-749-395	Sequence 395, App
44	66	47.8	260	9	US-09-918-585A-395	Sequence 395, App
45	66	47.8	260	9	US-10-143-032-396	Sequence 396, App

## ALIGNMENTS

### RESULT 1

US-09-938-269-1  
: Sequence 1, Application US/09938269  
: Publication NO. US20030007951A1  
: GENERAL INFORMATION:  
: APPLICANT: Franklin, Richard L.  
: APPLICANT: Cowling, Didier S.P.  
: APPLICANT: Hubbel, Jeffrey A.  
: APPLICANT: van de Wetering, Petra  
: TITLE OF INVENTION: Treatment of Trauma  
: FILE REFERENCE: 314572-105  
: CURRENT APPLICATION NUMBER: US/09/938, 269  
: CURRENT FILING DATE: 2001-08-23  
: NUMBER OF SEQ ID NOS: 17  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 1  
: LENGTH: 300  
: TYPE: PRT  
: ORGANISM: Panaeu vanameli  
: US-09-938-269-1

Query Match 98.6%; Score 136; DB 9; Length 300;  
Best Local Similarity 96.0%; Pred. NO. 5.1e-13;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY	1	IVGGXEVTPHAYPWQVGLFIDDMYF 25	
Db	64	IVGGMEVTPHAYPWQVGLFIDDMYF 88	

### RESULT 2

US-09-938-269-2  
: Sequence 2, Application US/09938269  
: Publication NO. US20030007951A1  
: GENERAL INFORMATION:  
: APPLICANT: Franklin, Richard L.  
: APPLICANT: Cowling, Didier S.P.  
: APPLICANT: Hubbel, Jeffrey A.  
: APPLICANT: van de Wetering, Petra  
: TITLE OF INVENTION: Treatment of Trauma  
: FILE REFERENCE: 314572-105  
: CURRENT APPLICATION NUMBER: US/09/938, 269

1 CURRENT FILING DATE: 2001-08-23  
1 NUMBER OF SEQ ID NOS: 17  
1 SOFTWARE: FastSeq for Windows Version 4.0  
1 SEQ ID NO 2  
1 LENGTH: 25  
1 TYPE: PRT  
1 ORGANISM: Panaeus vanamei  
US-09-938-269-2

Query Match 73.28; Score 101; DB 9; Length 25;  
Best Local Similarity 72.08; Pred. No. 7.9e-09;  
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQQAALFIDDMYF 25

US-09-938-269-6

Sequence 6, Application US/09938269  
Publication No. US20030007951A1

GENERAL INFORMATION:  
APPLICANT: Franklin, Richard L.  
APPLICANT: Cowling, Didier S.P.  
APPLICANT: Hubbel, Jeffrey A.  
TITLE OF INVENTION: Treatment of Trauma  
FILE REFERENCE: 314572-105  
CURRENT APPLICATION NUMBER: US/09/938,269  
CURRENT FILING DATE: 2001-08-23  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Panaeus monodon chymotryptic  
US-09-938-269-6

Query Match 65.98; Score 91; DB 9; Length 25;  
Best Local Similarity 64.08; Pred. No. 2.7e-07;  
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQQAALFIDDMYF 25

US-09-938-269-7

Sequence 7, Application US/09938269  
Publication No. US20030007951A1

GENERAL INFORMATION:  
APPLICANT: Franklin, Richard L.  
APPLICANT: Cowling, Didier S.P.  
APPLICANT: Hubbel, Jeffrey A.  
TITLE OF INVENTION: Treatment of Trauma  
FILE REFERENCE: 314572-105  
CURRENT APPLICATION NUMBER: US/09/938,269  
CURRENT FILING DATE: 2001-08-23  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Uca pugnator enzyme  
US-09-938-269-7

Query Match 64.5%; Score 89; DB 9; Length 25;  
Best Local Similarity 64.08; Pred. No. 5.4e-07;  
Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQQAALFIDDMYF 25

RESULT 5

US-09-938-269-5  
Sequence 5, Application US/09938269  
Publication No. US20030007951A1  
GENERAL INFORMATION:  
APPLICANT: Franklin, Richard L.  
APPLICANT: Cowling, Didier S.P.  
APPLICANT: Hubbel, Jeffrey A.  
TITLE OF INVENTION: Treatment of Trauma  
FILE REFERENCE: 314572-105  
CURRENT APPLICATION NUMBER: US/09/938,269  
CURRENT FILING DATE: 2001-08-23  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Panaeus monodon chymotryptic  
US-09-938-269-5

Query Match 58.08; Score 80; DB 9; Length 25;  
Best Local Similarity 60.08; Pred. No. 1.3e-05;  
Matches 15; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQQAALFIDDMYF 25

RESULT 6

US-09-888-615-101  
Sequence 101, Application US/09888615  
Patent No. US20020064856A1  
GENERAL INFORMATION:  
APPLICANT: PLOWMAN, GREGORY  
APPLICANT: WAYTE, DAVID  
APPLICANT: CAENEPEEL, SEAN  
APPLICANT: CHARYDCZAK, GLEN  
APPLICANT: MANNING, GERARD  
APPLICANT: SUDARSANAM, SUCHA  
TITLE OF INVENTION: NOVEL PROTEASES  
FILE REFERENCE: 038602/1214  
CURRENT APPLICATION NUMBER: US/09/888,615  
CURRENT FILING DATE: 2001-06-26  
PRIOR APPLICATION NUMBER: 60/214,047  
PRIOR FILING DATE: 2000-06-26  
NUMBER OF SEQ ID NOS: 150  
SOFTWARE: PatentIn ver. 2.1  
SEQ ID NO 101  
LENGTH: 970  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-888-615-101

Query Match 54.78; Score 75.5; DB 10; Length 970;  
Best Local Similarity 60.98; Pred. No. 0.0031;  
Matches 14; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 1 IVGGXVTPHAYPMQVGL-FIDD 22  
Db 433 IAGGEEACPHCWPMQVGLRFLGD 455

RESULT 7

US-10-117-323-37  
Sequence 37, Application US/10117323  
Publication No. US20030054993A1

```

: GENERAL INFORMATION:
: APPLICANT: Rancourt, Derrick E.
: APPLICANT: Rancourt, Susan L.
: APPLICANT: O'Sullivan, Colleen M.
: TITLE OF INVENTION: Implantation Serine Proteinases
: FILE REFERENCE: 03337-005
: CURRENT APPLICATION NUMBER: US/10/117,323
: CURRENT FILING DATE: 2002-04-08
: PRIOR FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: US 60/281,724
: PRIOR FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: US 60/294,736
: PRIOR FILING DATE: 2001-05-30
: PRIOR APPLICATION NUMBER: US 60/350,962
: PRIOR FILING DATE: 2002-01-25
: NUMBER OF SEQ ID NOS: 41
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 37
: LENGTH: 272
: TYPE: PRT
: ORGANISM: Mouse
: US-117-323-37

Query Match          50.7%  Score 70;  DB 9;  Length 272;
Best Local Similarity 48.0%  Pred. No. 0.0055;
Matches 12;  Conservative 6;  Mismatches 7;  Indels 0;  Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
    ||||| : : : ||||| : : : ||
Db 29 IVGGQEASGNKWPQVSLRVNDIYW 53

RESULT 8
US-10-117-323-39
: Sequence 39, Application US/10/117323
: Publication No. US20030054993A1
: GENERAL INFORMATION:
: APPLICANT: Rancourt, Derrick E.
: APPLICANT: Rancourt, Susan L.
: APPLICANT: O'Sullivan, Colleen M.
: TITLE OF INVENTION: Implantation Serine Proteinases
: FILE REFERENCE: 03337-005
: CURRENT APPLICATION NUMBER: US/10/117,323
: CURRENT FILING DATE: 2002-04-08
: PRIOR FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: US 60/281,724
: PRIOR FILING DATE: 2001-05-30
: PRIOR APPLICATION NUMBER: US 60/350,962
: PRIOR FILING DATE: 2002-01-25
: NUMBER OF SEQ ID NOS: 41
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 39
: LENGTH: 271
: TYPE: PRT
: ORGANISM: Mouse
: US-10-117-323-39

Query Match          50.0%  Score 69;  DB 9;  Length 271;
Best Local Similarity 61.1%  Pred. No. 0.0077;
Matches 11;  Conservative 3;  Mismatches 4;  Indels 0;  Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGL 18
    :||| : || : :||| :
Db 31 VVGQEATNTWPQVSL 48

RESULT 9
US-09-938-269-3
: Sequence 3, Application US/09938269
: Publication No. US20030007951A1
: GENERAL INFORMATION:
: APPLICANT: Franklin, Richard L.
: APPLICANT: Cowling, Didier S.P.

: GENERAL INFORMATION:
: APPLICANT: Hubbel, Jeffrey A.
: APPLICANT: van de Wetering, Petra
: FILE REFERENCE: 314572-105
: CURRENT APPLICATION NUMBER: US/09/938,269
: CURRENT FILING DATE: 2001-08-23
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Panaeus vanamei
: FEATURE:
: NAME/KEY: VARIANT
: LOCATION: (1)...(20)
: OTHER INFORMATION: Xaa - Any Amino Acid
: US-09-938-269-3

Query Match          49.3%  Score 68;  DB 9;  Length 20;
Best Local Similarity 65.0%  Pred. No. 0.00068;
Matches 13;  Conservative 1;  Mismatches 6;  Indels 0;  Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFI 20
    ||||| : ||| : |||
Db 1 IVGGVEATPHSXPHQAAALFI 20

RESULT 10
US-10-117-323-38
: Sequence 38, Application US/10/117323
: Publication No. US20030054993A1
: GENERAL INFORMATION:
: APPLICANT: Rancourt, Derrick E.
: APPLICANT: O'Sullivan, Colleen M.
: TITLE OF INVENTION: Implantation Serine Proteinases
: FILE REFERENCE: 03337-005
: CURRENT APPLICATION NUMBER: US/10/117,323
: CURRENT FILING DATE: 2002-04-08
: PRIOR APPLICATION NUMBER: US 60/281,724
: PRIOR FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: US 60/294,736
: PRIOR FILING DATE: 2001-05-30
: PRIOR APPLICATION NUMBER: US 60/350,962
: PRIOR FILING DATE: 2002-01-25
: NUMBER OF SEQ ID NOS: 41
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 38
: LENGTH: 252
: TYPE: PRT
: ORGANISM: Mouse
: US-10-117-323-38

Query Match          48.6%  Score 67;  DB 9;  Length 252;
Best Local Similarity 50.0%  Pred. No. 0.014;
Matches 9;  Conservative 5;  Mismatches 4;  Indels 0;  Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGL 18
    :||| : ||| : ||| :
Db 14 VVGEDARPHSWPQVSL 31

RESULT 11
US-09-898-837A-53
: Sequence 53, Application US/09898837A
: Publication No. US20030077697A1
: GENERAL INFORMATION:
: APPLICANT: Quinn, Kerry E.
: APPLICANT: Spytek, Kimberly A.
: APPLICANT: Majumder, Kumud
: APPLICANT: Vernet, Corine
: APPLICANT: Herrmann, John L.
: APPLICANT: Burgess, Catherine
```

APPLICANT: Fernandes, Elma  
APPLICANT: Taupier Jr., Raymond  
APPLICANT: Rastelli, Luca  
APPLICANT: CuraGen Corporation  
APPLICANT: Gerlach, Valerie L  
APPLICANT: Macdougall, John R  
TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND  
FILE REFERENCE: 15966-598 CIP  
CURRENT APPLICATION NUMBER: US/09/898,837A  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986  
PRIOR FILING DATE: 1999-11-17  
PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,839  
PRIOR FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080  
PRIOR FILING DATE: 2000-04-13  
PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347  
PRIOR FILING DATE: 2000-02-09  
PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195  
PRIOR FILING DATE: 2000-04-03  
PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906  
PRIOR FILING DATE: 2000-07-03  
PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 53  
LENGTH: 229  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-898-837A-53

Query Match 47.8%; Score 66; DB 9; Length 229;  
Best Local Similarity 45.8%; Pred. No. 0.019;  
Matches 11; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPNQVGLFIDDMY 24  
||||| | : ||||| | : : :  
Db 1 IVGGESALPGAWPQVSLHVQNVH 24

RESULT 12  
9-978-295A-395  
Sequence 395, Application US/09978295A  
Patent No. US20020156006A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
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PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
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PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
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PRIOR APPLICATION NUMBER: 60/079923  
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PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334

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US-09-978-697-395
: Sequence 395, Application US/09978697
: Patent No. US20020169284A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvarovff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goodard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James;
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and
: TITLE OF INVENTION: Acids Encoding

```

FILE REFERENCE: P2630P1C27  
 CURRENT APPLICATION NUMBER: US/09/978.697  
 CURRENT FILING DATE: 2001-10-16  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/064249  
 PRIOR FILING DATE: 1997-11-03  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
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 PRIOR FILING DATE: 1998-04-08  
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 PRIOR APPLICATION NUMBER: 60/084643

; PRIOR FILING DATE: 1998-05-07  
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 ; PRIOR FILING DATE: 1998-05-15  
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 ; PRIOR APPLICATION NUMBER: 60/085689  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085579  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085580  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085573  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085704  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 47.8%; Score 66; DB 9; Length 260;

Best Local Similarity 52.6%; Pred. No. 0.021;

Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 IVGGXVTPHAYPQVGLF 19  
 DB 33 VLGHECOPHSQPQQAALF 51  
 :||| | ||: ||| ||

# RESULT 14

US-09-978-192A-395  
 ; Sequence 395, Application US/09978192A  
 ; Patent No. US2002017553A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2630PIC9  
 ; CURRENT APPLICATION NUMBER: US/09/978,192A  
 ; CURRENT FILING DATE: 2001-10-15  
 ; PRIOR APPLICATION NUMBER: 09/918585  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249  
 ; PRIOR FILING DATE: 1997-11-03  
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 ; PRIOR FILING DATE: 1997-11-13  
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 ; PRIOR FILING DATE: 1998-04-01  
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 ; PRIOR APPLICATION NUMBER: 60/081070  
 ; PRIOR FILING DATE: 1998-04-08  
 ; PRIOR APPLICATION NUMBER: 60/081049  
 ; PRIOR FILING DATE: 1998-04-08  
 ; PRIOR APPLICATION NUMBER: 60/081071  
 ; PRIOR FILING DATE: 1998-04-08  
 ; PRIOR APPLICATION NUMBER: 60/081195  
 ; PRIOR FILING DATE: 1998-04-08  
 ; PRIOR APPLICATION NUMBER: 60/081203  
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 ; PRIOR FILING DATE: 1998-04-09  
 ; PRIOR APPLICATION NUMBER: 60/081955

;; PRIOR FILING DATE: 1998-04-15  
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;; PRIOR APPLICATION NUMBER: 60/081819  
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;; PRIOR APPLICATION NUMBER: 60/081952  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/081838  
;; PRIOR FILING DATE: 1998-04-15  
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;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083559  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083500  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083742  
;; PRIOR FILING DATE: 1998-04-30  
;; PRIOR APPLICATION NUMBER: 60/084366  
;; PRIOR FILING DATE: 1998-05-05  
;; PRIOR APPLICATION NUMBER: 60/084414  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084441  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084637  
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;; PRIOR APPLICATION NUMBER: 60/085582  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085689  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
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;; PRIOR FILING DATE: 1998-05-15  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 47.8%; Score 66; DB 9; Length 260;  
Best Local Similarity 52.6%; Pred. No. 0.021;  
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPMOVGLF 19  
Db 33 VLGGHCOPHSQPMQAAALF 51

RESULT 15  
US-09-999-832A-395  
; Sequence 395 Application US/09999832A  
; Publication No. US20020192706A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC63  
; CURRENT APPLICATION NUMBER: US/09/999,832A  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450



1	PRIOR APPLICATION NUMBER: 60/081833
2	PRIOR FILING DATE: 1998-04-15
3	PRIOR APPLICATION NUMBER: 60/082568
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8	PRIOR FILING DATE: 1998-04-22
9	PRIOR APPLICATION NUMBER: 60/082804
10	PRIOR FILING DATE: 1998-04-22
11	PRIOR APPLICATION NUMBER: 60/082700
12	PRIOR FILING DATE: 1998-04-22
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14	PRIOR FILING DATE: 1998-04-22
15	PRIOR APPLICATION NUMBER: 60/082796
16	PRIOR FILING DATE: 1998-04-23
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18	PRIOR FILING DATE: 1998-04-27
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33	PRIOR APPLICATION NUMBER: 60/083558
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35	PRIOR APPLICATION NUMBER: 60/083559
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41	PRIOR APPLICATION NUMBER: 60/084366
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49	PRIOR APPLICATION NUMBER: 60/084639
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51	PRIOR APPLICATION NUMBER: 60/084640
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53	PRIOR APPLICATION NUMBER: 60/084598
54	PRIOR FILING DATE: 1998-05-07
55	PRIOR APPLICATION NUMBER: 60/084600
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57	PRIOR APPLICATION NUMBER: 60/085339
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59	PRIOR APPLICATION NUMBER: 60/085338
60	PRIOR FILING DATE: 1998-05-13
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64	PRIOR FILING DATE: 1998-05-15
65	PRIOR APPLICATION NUMBER: 60/085700
66	PRIOR FILING DATE: 1998-05-15
67	PRIOR APPLICATION NUMBER: 60/085689
68	PRIOR FILING DATE: 1998-05-15
69	PRIOR APPLICATION NUMBER: 60/085579

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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Query Match      47.8%; Score 66; DB 9; Length 260;
Best Local Similarity 52.6%; Pred. NO. 0.021;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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QY      1 IVGGXEVTPHAYPQVGLF 19
Db      33 VLGHECQPHSQPWQAALF 51

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ch completed: May 30, 2003, 11:13:13

Time : 46 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 10:50:27 ; Search time 22 Seconds  
(without alignments)  
47.132 Million cell updates/sec

Title: US-09-549-642-20  
Perfect score: 138  
Sequence: 1 IVGXEVTTPHAYPMQVGLFIDMYF 25

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Number of hits satisfying chosen parameters: 112892

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	73.2	271	1	Q00871 penaeus van
2	101	73.2	271	1	P36178 penaeus van
3	89	64.5	226	1	P00771 uca pugil
4	80	58.0	31	1	P35002 penaeus mon
5	70	50.7	273	1	P27435 rattus norv
6	69	50.0	271	1	P05208 mus musculu
7	69	50.0	343	1	P81286 ovis aries
8	67	48.6	245	1	P80646 gadus morhu
9	67	48.6	268	1	Q99895 homo sapien
10	67	48.6	275	1	Q9n2d1 sus scrofa
11	66	47.8	260	1	O60259 homo sapien
12	66	47.8	271	1	P00774 rattus norv
13	66	47.8	492	1	O15393 homo sapien
14	65	47.1	20	1	P34153 chionocete
15	65	47.1	262	1	P12544 homo sapien
16	64	46.4	269	1	P08217 homo sapien
17	63	45.7	20	1	P07331 paralithode
18	63	45.7	269	1	P08419 sus scrofa
19	63	45.7	273	1	Q02844 mus musculu
20	63	45.7	273	1	Q9xsm2 ovis aries
21	63	45.7	275	1	P15157 homo sapien
22	63	45.7	333	1	P00009 canis fami
23	63	45.7	812	1	P06868 bos taurus
24	63	45.7	812	1	P20918 mus musculu
25	63	45.7	1420	1	P14417 macaca mula
26	63	45.7	4548	1	P08519 homo sapien
27	62	44.9	254	1	Q9y5k2 homo sapien
28	62	44.9	268	1	P55091 rattus norv
29	62	44.9	810	1	P00747 homo sapien
30	61	44.2	250	1	Q9ubx7 homo sapien
31	61	44.2	269	1	Q29461 bos taurus
32	61	44.2	810	1	P12545 macaca mula
33	61	44.2	1035	1	P36072 bos taurus

RESULT 1  
CTRL\_PENVA  
ID CTRL\_PENVA STANDARD: PRT: 271 AA.  
AC Q00871;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Chymotrypsin BI precursor (EC 3.4.21.1).  
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;  
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata;  
OC Penaeoidea; Penaeidae; Litopenaeus.  
OX NCBI\_TaxID=6689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hepatopancreas;  
RX MEDLINE=92387359; PubMed=1516690;  
RA Sellos D.; van Wormhoudt A.;  
RT "Molecular cloning of a cDNA that encodes a serine protease with  
chymotryptic and collagenolytic activities in the hepatopancreas of  
the shrimp Penaeus vannamei (Crustacea, Decapoda).";  
RL FEBS Lett. 309:219-224(1992).  
RN [2]  
RP SEQUENCE OF 46-65, AND CHARACTERIZATION.  
RC TISSUE=Hepatopancreas;  
RX MEDLINE=93092601; PubMed=1458841;  
RA van Wormhoudt A.; le Chevalier P.; Sellos D.;  
RT "Purification, biochemical characterization and N-terminal sequence  
of a serine-protease with chymotryptic and collagenolytic activities  
in a tropical shrimp, Penaeus vannamei (Crustacea, Decapoda).";  
RL Comp. Biochem. Physiol. 103B:675-680(1992).  
CC -!- FUNCTION: SERINE PROTEASE WITH CHYMOTRYPTIC AND COLLAGENOLYTIC  
ACTIVITIES.  
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-I-Xaa, Trp-I-Xaa,  
Phe-I-Xaa, Leu-I-Xaa.  
CC -!- SUBCELLULAR LOCATION: Extracellular.  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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entities requires a license agreement (see http://www.isb-sib.ch/announce/  
or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL: X66415; CAA47046.1; -  
CC PIR: S22075; S22075.  
CC PIR: S29239; S29239.  
CC HSP: P00771; IAZZ.  
CC MEROPS: S01.121; -  
CC InterPro: IPR001314; Chymotrypsin.  
CC InterPro: IPR001254; Ser-protease\_Try.  
CC Pfam: PF00089; trypsin; 1  
CC PRINTS: PR00722; CHYMOTRYPSIN.  
CC SMART: SM00020; Tryp\_Spc; 1.  
CC -----

#### ALIGNMENTS

P50342 meriones un  
Q91iq8 mus musculu  
P06867 sus scrofa  
Q9h2r5 homo sapien  
Q61955 mus musculu  
O88780 rattus norv  
P28293 mus musculu  
P20151 homo sapien  
P47796 gadus morhu  
P08218 homo sapien  
Q29485 erinaceus e  
Q9ukq9 homo sapien

1 TRYT\_MERUN  
1 TMS2\_MOUSE  
1 PLMN\_PIG  
1 KLKF\_HUMAN  
1 NRPN\_MOUSE  
1 NRPN\_RAT  
1 CATG\_MOUSE  
1 KLK2\_HUMAN  
1 CTRA\_GADMO  
1 EL2B\_HUMAN  
1 PLMN\_ERIEU  
1 KLK9\_HUMAN

60 43.5 270 1  
35 60 43.5 490 1  
36 60 43.5 790 1  
37 59 42.8 256 1  
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42 59 42.8 263 1  
43 59 42.8 269 1  
44 59 42.8 810 1  
45 58 42.0 250 1

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DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Zymogen; Signal; Multigene family.
FT SIGNAL 1 15
FT PROPEP 16 45
FT CHAIN 46 271
FT ACT_SITE 86 86
FT ACT_SITE 132 132
FT ACT_SITE 223 223
FT ACT_SITE 223 223
FT DISULFID 71 87
FT DISULFID 196 209
FT DISULFID 219 245
SQ SEQUENCE 271 AA; 28685 MW; 0967398D5401E5B7 CRC64;

Query Match 73.2%; Score 101; DB 1; Length 271;
Best Local Similarity 72.0%; Pred. No. 6e-08;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

1 IVGXEVTTPHAYPMQVGLFIDDMYF 25
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46 IVGVEATPHSNPQAAALFIDDMYF 70

RESULT 2
ID CTR2_PENVA STANDARD; PRT; 271 AA.
AC P36178;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chymotrypsin BII precursor (EC 3.4.21.1).
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea; Penaeidae; Litopenaeus.
OC NCBI_TaxID=6689;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Hepatopancreas;
RX MEDLINE=92387359; PubMed=1516690;
RA Sellos D., van Wormhoudt A.;
RT "Molecular cloning of a cDNA that encodes a serine protease with chymotryptic and collagenolytic activities in the hepatopancreas of the shrimp Penaeus vannamei (Crustacea, Decapoda).";
RL FEBS Lett. 309:219-224(1992).
RN [2]
CC SEQUENCE OF 46-65, AND CHARACTERIZATION.
CC TISSUE-Hepatopancreas;
CC MEDLINE=9302601; PubMed=1458841;
RA van Wormhoudt A., le Chevallier P., Sellos D.;
RT "Purification, biochemical characterization and N-terminal sequence of a serine-protease with chymotryptic and collagenolytic activities in a tropical shrimp, Penaeus vannamei (Crustacea, Decapoda).";
RL Comp. Biochem. Physiol. 103B:675-680(1992).
CC -1- FUNCTION: SERINE PROTEASE WITH CHYMOTRYPTIC AND COLLAGENOLYTIC ACTIVITIES.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-I-Xaa, Trp-I-Xaa, Phe-I-Xaa, Leu-I-Xaa.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR HSP. P00771; IAZZ.
DR MEROPS; S01.121; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser.protease_try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Zymogen; Signal; Multigene family.
FT SIGNAL 1 15
FT
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FT PROPEP 16 45
FT CHAIN 46 271
FT ACT_SITE 86 86
FT ACT_SITE 132 132
FT ACT_SITE 223 223
FT DISULFID 71 87
FT DISULFID 196 209
FT DISULFID 219 245
SQ SEQUENCE 271 AA; 28723 MW; 225407C7E663FA2E1 CRC64;

Query Match 73.2%; Score 101; DB 1; Length 271;
Best Local Similarity 72.0%; Pred. No. 6e-08;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

1 IVGXEVTTPHAYPMQVGLFIDDMYF 25
||||| ||||| ||||| ||||| |||||
46 IVGVEATPHSNPQAAALFIDDMYF 70

RESULT 3
ID COGS_UCAPU STANDARD; PRT; 226 AA.
AC P00771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Brachyurin (EC 3.4.21.32) (Collagenolytic protease).
OS Uca pugnator (Atlantic sand fiddler crab) (Celuca pugnator).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Ocypodoidea; Ocypodidae; Ocypodinae; Uca complex; Celuca.
OC NCBI_TaxID=6772;
OX [1]
RN [1]
RP SEQUENCE.
RC TISSUE-Hepatopancreas;
RX MEDLINE=81040004; PubMed=6252953;
RA Grant G.A., Henderson K.O., Eisen A.Z., Bradshaw R.A.;
RT "Amino acid sequence of a collagenolytic protease from the hepatopancreas of the fiddler crab, Uca pugnator.";
RL Biochemistry 19:4653-4659(1980).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS). AND REVISIONS.
RC TISSUE-Hepatopancreas;
RX MEDLINE=97299771; PubMed=9154920;
RA Perona J.J., Tsu C.A., Craik C.S., Fletterick R.J.;
RT "Crystal structure of an ecotin-collagenase complex suggests a model for recognition and cleavage of the collagen triple helix.";
RL Biochemistry 36:5381-5392(1997).
CC -1- FUNCTION: THIS ENZYME IS A SERINE PROTEASE CAPABLE OF DEGRADING THE NATIVE TRIPLE HELIX OF COLLAGEN.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of proteins, with broad specificity for peptide bonds. Degrades native collagen at about 75% of the length of the molecule from the N-terminus. Low activity on small molecule substrates of both trypsin and chymotrypsin.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR PIR; A00958; KCUF.
DR PDB; 1AZZ; 25-FEB-98.
DR MEROPS; S01.122; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser.protease_try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Collagen degradation; 3D-structure.
FT ACT_SITE 41 87
FT ACT_SITE 87 87
FT ACT_SITE 178 178
FT ACT_SITE 26 42
FT DISULFID 26 42
FT DISULFID 151 164
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FT DISULFID 218 246 BY SIMILARITY.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CONFLICT 42 42 W -> V (IN REF. 3).
FT CONFLICT 49 51 NDT -> WLP (IN REF. 3).
SQ SEQUENCE 273 AA; 30400 MW; 65A5ED4D279FB284 CRC64;

Query Match 50.7%; Score 70; DB 1; Length 273;
Best Local Similarity 48.0%; Pred. No. 0.0027;
Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 IVGGXVTPHAYPNQVCLFDDMYF 25
    ||||| : : ||||| : : || :
Db 29 IVGGQASGNKWPQVSLRVNDTYW 53

RESULT 6
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P05208;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elastase 2 precursor (EC 3.4.21.71).
GN ELA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87066713; PubMed=3641189;
RA Stevenson B.J., Hagenbuechle O., Wellauer P.K.;
RT "Sequence organisation and transcriptional regulation of the mouse
RT elastase II and trypsin genes.";
RL Nucleic Acids Res. 14:8307-8330(1986).
CC -1- FUNCTION: ACTS UPON ELASIN.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Leu-I-Xaa, Met-I-Xaa
CC and Phe-I-Xaa. Hydrolyzes elastin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; X04573; CAA28242.1; .
DR EMBL; X04576; CAA28244.1; .
DR PIR; A25528; A25528.
DR HSP; P00772; IELG.
DR MEROPS; S01.155; .
DR MGD; MGI:95316; Ela2.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; trypsin; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; zymogen; Signal.
FT SIGNAL 1 16
FT PROPEP 17 30 ACTIVATION PEPTIDE.
FT CHAIN 31 271 ELASTASE 2.
FT ACT_SITE 75 75 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 123 123 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 218 218 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 60 76 BY SIMILARITY.
FT DISULFID 157 224 BY SIMILARITY.

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FT DISULFID 188 204 BY SIMILARITY.
FT DISULFID 214 245 BY SIMILARITY.
SQ SEQUENCE 271 AA; 28913 MW; FA542AE38FED3B4B CRC64;

Query Match 50.0%; Score 69; DB 1; Length 271;
Best Local Similarity 61.1%; Pred. No. 0.0037;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 IVGGXVTPHAYPNQVGL 18
    ||||| : : ||||| :
Db 31 VVGQEQATPNTWPQVSL 48

RESULT 7
PLMN_SHEEP STANDARD; PRT; 343 AA.
AC P81286;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
GN PLG.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=93149995; PubMed=1492092;
RA Schaller J., Straub C., Kampfer U., Rickli E.E.;
RT "Complete amino acid sequence of ovine miniplasminogen.";
RL Protein Seq. Data Anal. 5:21-25(1992).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-I-Xaa > Arg-I-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: CONTAINS AT LEAST 2 KRINGLE DOMAINS.
DR HSP; P00747; 5HPG.
DR MEROPS; S01.233; .
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; K8; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
FT NON_TER 1 1
FT DOMAIN <1 140 HEAVY CHAIN A.
FT DOMAIN 141 >343 LIGHT CHAIN A.
FT DOMAIN <1 17 KRINGLE 4.
FT DOMAIN 41 120 KRINGLE 5.
FT DOMAIN 114 341 SERINE PROTEASE.

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FT ACT\_SITE 181 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 224 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 319 CHARGE RELAY SYSTEM.  
 FT NON\_TER 343  
 SQ SEQUENCE 343 AA: 37662 MW; 8DF6EBA92D596EE0 CRC64;

Query Match 50.0%; Score 69; DB 1; Length 343;  
 Best Local Similarity 61.1%; Pred. No. 0.0047;  
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 IVGXEVTPTPHAYPMQVGL 18  
 :111 111:11111  
 Db 114 VVGCVATPHSWPMQVSL 131

RESULT 8  
 CTRB\_GADMO  
 ID CTRB\_GADMO STANDARD; PRT; 245 AA.  
 AC P80646;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 Chymotrypsin B (EC 3.4.21.1).  
 GADMO morhua (Atlantic cod).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorphi; Paracanthopterygii; Gadiformes; Gadidae; Gadus.  
 OX NCBI\_TaxID=8049;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pyloric caeca;  
 RX MEDLINE=96439045; PubMed=8841380;  
 RA Leth-Larsen R., Asgerlsson B., Thorolfsson M., Noerregaard-Madsen M.,  
 RA Hoejrup P.;  
 RT "Structure of chymotrypsin variant B from Atlantic cod, Gadus  
 morhua.";  
 RL Biochim. Biophys. Acta 1297:49-56(1996).  
 RN [2]  
 RP SEQUENCE OF 1-12 AND 16-31.  
 RC TISSUE=Pyloric caeca;  
 RX MEDLINE=92111252; PubMed=1764912;  
 RA Asgerlsson B., Bjarnason J.B.;  
 RT "Structural and kinetic properties of chymotrypsin from Atlantic cod  
 (Gadus morhua). Comparison with bovine chymotrypsin.";  
 RL Comp. Biochem. Physiol. 99B:327-335(1991).  
 CC [1]  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-I-Xaa, Trp-I-Xaa,  
 Phe-I-Xaa, Leu-I-Xaa.  
 CC -1- SUBCELLULAR LOCATION: Extracellular.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 HSSP: P00766; 1CHG.  
 MEROPS: S01.152; .

DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYP\_SPE; 1.  
 DR PROSITE: PS02040; TRYPIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPIN\_SER; 1.  
 KW Hydrolase; Serine protease; Digestion; Pancreas; Zymogen.  
 FT CHAIN 1 13  
 FT CHAIN 16 245  
 CHYMOTRYPSIN B, A CHAIN.  
 CHYMOTRYPSIN B, B CHAIN.  
 FT ACT\_SITE 57 57  
 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 101 101  
 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 195 195  
 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 1 121  
 BY SIMILARITY.  
 FT DISULFID 42 58  
 BY SIMILARITY.  
 FT DISULFID 135 201  
 BY SIMILARITY.  
 FT DISULFID 167 182  
 BY SIMILARITY.  
 FT DISULFID 191 220  
 BY SIMILARITY.  
 FT CONFLICT 9 11  
 QVT -> VIS (IN REF. 2).  
 FT CONFLICT 26 26  
 S -> T (IN REF. 2).  
 FT CONFLICT 28 29  
 PW -> Y (IN REF. 2).

SQ SEQUENCE 245 AA: 26260 MW; 74FE0D425517AB02 CRC64;  
 Query Match 48.6%; Score 67; DB 1; Length 245;  
 Best Local Similarity 61.1%; Pred. No. 0.0067;  
 Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 IVGXEVTPTPHAYPMQVGL 18  
 :111 111:11111  
 Db 16 IVNGEAVPHSWPMQVSL 33

RESULT 9  
 CLCR\_HUMAN  
 ID CLCR\_HUMAN STANDARD; PRT; 268 AA.  
 AC Q99895; Q9NUH5; Q00765;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Caldecrin precursor (EC 3.4.21.2) (Chymotrypsin C).  
 GN CTRC OR CLCR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND VARIANT TRP-80.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=96221265; PubMed=8635596;  
 RA Tomomura A., Akiyama M., Itoh H., Yoshino I., Tomomura M., Nishii Y.,  
 RA Nolkura T., Saheki T.;  
 RT "Molecular cloning and expression of human caldecrin.";  
 RL FEBS Lett. 386:26-28(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Coville G.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 17-268 FROM N.A.  
 RC TISSUE=Pancreas;  
 RA Sziegoleit A.;  
 RT "A human pancreatic chymotrypsin: biochemical and molecular  
 characterization.";  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP CHARACTERIZATION.  
 RX MEDLINE=98207038; PubMed=9538241;  
 RA Yoshino-Yasuda I., Kobayashi K., Akiyama M., Itoh H., Tomomura A.,  
 RA Saheki T.;  
 RT "Caldecrin is a novel-type serine protease expressed in pancreas, but  
 its homologue, elastase IV, is an artifact during cloning derived  
 from caldecrin gene.";  
 RL J. Biochem. 123:546-554(1998).  
 CC [1]  
 CC -1- FUNCTION: HAS CHYMOTRYPSIN-TYPE PROTEASE ACTIVITY AND HYPOCALCEMIC  
 ACTIVITY.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Leu-I-Xaa, Tyr-I-Xaa,  
 Phe-I-Xaa, Met-I-Xaa, Trp-I-Xaa, Glu-I-Xaa, Asn-I-Xaa.  
 CC -1- TISSUE SPECIFICITY: PANCREAS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.  
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 CC -----  
 EMBL; S82198; AAB47104.2; ALT\_SEQ.  
 EMBL; AL031283; CAB77355.1; .  
 EMBL; Y13697; CAA74031.1; .  
 HSSP: P00766; 1CHG.  
 MEROPS: S01.157; .  
 Genew; HGNC:2523; CTRC.

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DR MM: 601405;
DR InterPro: IPR001314; Chymotrypsin.
DR Pfam: PF00089; trypsin; 1
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP-SPC; 1.
DR PROSITE: PS00240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
KW Polymorphism.
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 29 ACTIVATION PEPTIDE.
FT CHAIN 30 268 CALDECRIN.
FT ACT_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 216 216 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 17 141 BY SIMILARITY.
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 155 222 BY SIMILARITY.
FT DISULFID 186 202 BY SIMILARITY.
FT DISULFID 212 243 BY SIMILARITY.
FT CARBOHYD 25 25 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 52 52 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 80 80 R -> W.
FT CONFLICT 16 16 S -> T (IN REF. 1).
FT CONFLICT 52 52 N -> D (IN REF. 3).
SQ SEQUENCE 268 AA; 29484 MW; 460BF3B4A96516F CRC64;

Query Match 48.6%; Score 67; DB 1; Length 268;
Best Local Similarity 50.0%; Pred. No. 0.0073;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPQVGL 18
DB 30 VVGEDARHPWPQISL 47

RESULT 10
TRYTP_PIG
ID TRYTP_PIG STANDARD; PRT; 275 AA.
AC Q9N2D1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Trypsin precursor (EC 3.4.21.59).
DE MCTV.
DE Sus scrofa (Pig).
DE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
DE NCBI_TaxID=9823;
DE [1]
DE SEQUENCE FROM N.A.
DE TISSUE=Lung;
DE MEDLINE=20285343; PubMed=10824103;
DE Chen Y., Shiota M., Ohuchi M., Towatari T., Tashiro J., Murakami M.,
DE Yano M., Yang B., Kido H.;
DE "Mast cell tryptase from pig lungs triggers infection by pneumotropic
DE Sendai and influenza A viruses. Purification and characterization."
DE Eur. J. Biochem. 267:3189-3197(2000).
DE CC -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
DE CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
DE RESPONSE OF THIS CELL TYPE.
DE CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
DE which more restricted specificity than trypsin.
DE CC -!- SUBUNIT: HOMOTETRAMER (By similarity).
DE CC -!- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
DE MAST CELL ACTIVATION.
DE CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
DE CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AB038652; BAA93614.1;
CC HSSP: P20231; IMAO.
CC MEROPS: S01.143;
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR001254; Ser_protease_Try.
CC Pfam: PF00089; trypsin; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC SMART: SM00020; TRYP-SPC; 1.
CC PROSITE: PS00240; TRYPsin_DOM; 1.
CC PROSITE: PS00134; TRYPsin_HIS; 1.
CC PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Zymogen.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 30 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 31 275 TRYPTASE.
FT ACT_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 224 224 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 155 230 BY SIMILARITY.
FT DISULFID 188 211 BY SIMILARITY.
FT DISULFID 220 248 BY SIMILARITY.
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 275 AA; 30439 MW; ACC583647FCCB973 CRC64;

Query Match 48.6%; Score 67; DB 1; Length 275;
Best Local Similarity 52.0%; Pred. No. 0.0075;
Matches 13; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPQVGLFIDDMYF 25
DB 31 IVGKEAPGHKWPQVSLRCLDQYW 55

RESULT 11
KLK8_HUMAN
ID KLK8_HUMAN STANDARD; PRT; 260 AA.
AC O60259; Q9UQ47; Q9HCB3; Q9U1L9;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neutrophin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Ovasin) (Serine
DE protease TADG-14) (Tumor-associated differentially expressed gene-14
DE protein).
DE GN KLK8 OR PRSS19 OR TADG14 OR NRPN.
DE OS Homo sapiens (Human).
DE OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
DE NCBI_TaxID=9606;
DE [1]
DE SEQUENCE FROM N.A. (ISOFORM 1).
DE TISSUE=Hippocampus;
DE MEDLINE=98372070; PubMed=9714609;
DE Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;
DE "Sequence analysis and expression of human neutrophin CDNA and gene.";
DE Gene 213:9-16(1998).
DE [2]
DE SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
DE TISSUE=Brain;
DE MEDLINE=99203457; PubMed=10102990;
DE Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
DE "A novel form of human neutrophin, a brain-related serine protease, is
DE generated by alternative splicing and is expressed preferentially in
DE human adult brain.";
DE Eur. J. Biochem. 260:627-634(1999).

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RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Ovary;  
 RX MEDLINE=99413504; PubMed=10485494;  
 RA Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,  
 RA O'Brien T.J.;  
 RT "Cloning of tumor-associated differentially expressed gene-14, a novel  
 RT serine protease overexpressed by ovarian carcinoma.";  
 RL Cancer Res. 59:4435-4439(1999).  
 RN [4]  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Gen L., Gellinas R., Gown A.M., Moss P., Smith R., Wang K.;  
 RT "Molecular cloning and characterization of a novel serine protease,  
 RT ovasin, a potential molecular marker for ovarian carcinomas.";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RA MEDLINE=20510030; PubMed=11054574;  
 RX Moss P., Paepfer B., Wang K.;  
 RA Gen L., Lee I., Smith R., Agonza-Barrett R., Lei H., McCuaig J.,  
 RA "Sequencing and expression analysis of the serine protease gene  
 RA cluster located in chromosome 19q13 region.";  
 RL Gene 257:119-130(2000).  
 RN [6]  
 RN SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).  
 RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,  
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,  
 RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,  
 RA Andreise T., Trankhelm M., Attix C., Amico-Keller G., Coefield J.,  
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,  
 RA Arellano A., Sanders C., Ow D., Nolan P., Trong S., Kobayashi A.,  
 RA Olsen A.S., Carrano A.V.;  
 RT "Sequence analysis of chromosome 19q13.4.";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RN FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND  
 CC HIPPOCAMPAL PLASTICITY.  
 CC  
 CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-.  
 CC  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2: ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC  
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS PREDOMINANTLY EXPRESSED IN THE  
 CC PANCREAS WHILE ISOFORM 2 IS EXPRESSED IN ADULT BRAIN AND  
 CC HIPPOCAMPUS. BOTH FORMS ARE ALSO FOUND IN FETAL BRAIN AND  
 CC PLACENTA. NOT DETECTED IN KIDNEY, SPLEEN, LIVER AND LUNG.  
 CC  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.  
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 CC -----  
 CC EMBL: AB009849; BAA28673.1;  
 CC EMBL: AB012761; BAA28676.1;  
 CC EMBL: AB010780; BAA88684.1;  
 CC EMBL: AB008390; BAA82665.1;  
 CC EMBL: AB008927; BAA82666.1;  
 CC EMBL: AF055982; AAD56050.1;  
 CC EMBL: AF095742; AAD25979.1;  
 CC EMBL: AF095743; AAD29574.1;  
 CC EMBL: AF243527; AAG33361.1;  
 CC EMBL: AC011473; AAG23254.1;  
 CC HSSP: O61955; 1NPM.  
 CC MEROPS: S01.244;  
 CC Genew: HGNC:6369; KLR8.  
 CC MIM: 605644;  
 CC InterPro: IPR001314; Chymotrypsin.  
 CC InterPro: IPR001254; Ser.protease\_Try.  
 CC Pfam: PF00089; trypsin; 1.  
 CC PRINTS: PR00722; CHYMOTRYPsin.

DR SMART: SM00020; Tryp\_SPC: 1.  
 DR PROSITE: PS0240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;  
 KW Alternative splicing.  
 FT SIGNAL 1 28 POTENTIAL.  
 FT PROPEP 29 32 BY SIMILARITY.  
 FT CHAIN 33 260 NEUROPSIN.  
 FT ACT\_SITE 73 73 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 39 173 BY SIMILARITY.  
 FT DISULFID 58 74 BY SIMILARITY.  
 FT DISULFID 145 246 BY SIMILARITY.  
 FT DISULFID 152 218 BY SIMILARITY.  
 FT DISULFID 184 198 BY SIMILARITY.  
 FT DISULFID 208 233 BY SIMILARITY.  
 FT CARBOHYD 110 110 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT VARSPIC 23 23 WRSNPLPPAA (IN ISOFORM 2).  
 SQ SEQUENCE 260 AA; 28048 MW; EF439E5B8C83E660 CRC64;  
 Query Match 47.8%; Score 66; DB 1; Length 260;  
 Best Local Similarity 52.8%; Pred. No. 0.01;  
 Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 IVGGXEVTPHAYVQVGLF 19  
 DB 33 VLGGHECQPHSQPWQAALF 51  
 RESULT 12  
 EL2 RAT  
 ID EL2 RAT STANDARD; PRT; 271 AA.  
 AC P00774;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Elastase 2 precursor (EC 3.4.21.71).  
 GN ELA2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=101116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82182957; PubMed=6918221;  
 RA McDonald R.J., Swift G.H., Quinto C., Swain W., Pictet R.L.,  
 RA Nikovits W., Rutter W.J.;  
 RT "Primary structure of two distinct rat pancreatic preproelastases  
 RT determined by sequence analysis of the complete cloned messenger  
 RT ribonucleic acid sequences.";  
 RL Biochemistry 21:1453-1463(1982).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=85054882; PubMed=6094548;  
 RA Swift G.H., Craik C.S., Stary S.J., Quinto C., Lahate R.G.,  
 RA Rutter W.J., Macdonald R.J.;  
 RT "Structure of the two related elastase genes expressed in the rat  
 RT pancreas.";  
 RL J. Biol. Chem. 259:14271-14278(1984).  
 CC -1- FUNCTION: ACTS UPON ELASTIN.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Met-|-Xaa  
 CC and Phe-|-Xaa. Hydrolyzes elastin.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: PANCREAS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.  
 CC -----  
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4. HUMAN STANDARD; PRT; 262 AA.

T-1989 (Rel. 12, Created)  
T-1989 (Rel. 12, Last sequence update)  
N-2002 (Rel. 41, Last annotation update)  
T-lyme A precursor (EC 3.4.21.78) (Cytotoxic T-lymphocyte proteinase)  
manukah factor) (H factor) (HF) (Granzyme 1) (CTL tryptase)  
1).  
OR CTLA3 OR HFSP.  
sapiens (Human).  
oyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TaxID=9606;

NCE FROM N.A.  
E-T-cell.  
N-88125000; PubMed=3257574;  
H.K., Hershberger R.J., Shows T.B., Weissman I.L.;  
ing and chromosomal assignment of a human cDNA encoding a T  
and natural killer cell-specific trypsin-like serine  
ase";  
Natl. Acad. Sci. U.S.A. 85:1184-1188(1988).

NCE FROM N.A.  
E-Blood;  
Hershberger R.;  
titled (OCT-2001) to the EMBL/GenBank/DBJ databases.

NCE OF 1-23 FROM N.A.  
Ski T.J., Krensky A.M.;  
upstream region of the human granzyme A locus contains both  
positive and negative transcriptional regulatory elements";  
titled (NOV-1995) to the EMBL/GenBank/DBJ databases.

NCE OF 29-53.  
N-88330824; PubMed=3047119;  
Bennett C.D., Biddison W.E., Blake J.T., Norton G.P.,  
J.Y. J.A., Sigal N.H., Turner R.V., Wu J.K., Zwerink H.J.;  
n cytotoxic lymphocyte tryptase. Its purification from granules  
the characterization of inhibitor and substrate specificity";  
bl. Chem. 263:13215-13222(1988).

NCE OF 29-40, AND CHARACTERIZATION.  
N-89009866; PubMed=3262682;  
d A., Lowrey D.M., Lichtenheld M., Podack E.R.;  
acterization of three serine esterases isolated from human IL-2  
ated killer cells";  
munol. 141:3142-3147(1988).

NCE OF 29-39, AND CHARACTERIZATION.  
N-89035468; PubMed=3233427;  
enbuhl O., Rey C., Jenne D.E., Lanzavecchia A., Groscurth P.,  
l S., Tschopp J.;  
acterization of granzymes A and B isolated from granules of  
d human cytotoxic T lymphocytes";  
munol. 141:3471-3477(1988).

STRUCTURE MODELING.  
N-89184501; PubMed=32337717;  
y M.E.P., Moutl J., Bleackley R.C., Gershenfeld H.,  
an I.L., James M.N.G.;  
ative molecular model building of two serine proteinases from  
oxic T lymphocytes.";  
ins 4:190-204(1988).  
UNCTION: THIS ENZYME IS NECESSARY FOR TARGET CELL LYSIS IN CELL-  
MEDIATED IMMUNE RESPONSES. IT CLEAVES AFTER LYS OR ARG. MAY BE  
INVOLVED IN APOPTOSIS.  
CATALYTIC ACTIVITY: Hydrolysis of proteins, including fibronectin,  
type IV collagen and nucleolin. Preferential cleavage: Arg-I-Xaa,  
ys-I-Xaa >> Phe-I-Xaa in small molecule substrates.  
SUBUNIT: HOMODIMER; DISULFIDE-LINKED.

```

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC GRANULES.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. GRANZYME SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL: M18737; AAS2647.1;
CC EMBL: BC015739; AAH15739.1;
CC EMBL: U40006; AAD00009.1;
CC PIR: A28943; A28943.
CC PIR: A30525; A30525.
CC PIR: A30526; A30526.
CC PIR: A31372; A31372.
CC PDB: 1HFI; 15-OCT-94.
CC MEROPS: S01.135;
CC Genew: HGNC:4708; GZMA.
CC MIM: 140050;
CC InterPro: IPR001254; Ser_protease_Try.
CC Pfam: PF00089; trypsin; 1.
CC SMART: SM00020; TRYP_SPC; 1.
CC PROSITE: PS00240; TRYPsin_DOM; 1.
CC PROSITE: PS00134; TRYPsin_HIS; 1.
CC PROSITE: PS00135; TRYPsin_SER; 1.
CC Hydrolase; Serine protease; Zymogen; Signal; T-cell; Cytolysis;
CC Apoptosis; 3D-structure.
FT SIGNAL 1 26
FT PROPEP 27 28
FT CHAIN 29 262
FT ACT_SITE 69 69
FT ACT_SITE 114 114
FT ACT_SITE 212 212
FT DISULFID 54 70
FT DISULFID 148 218
FT DISULFID 179 197
FT DISULFID 208 234
FT CARBOHYD 170 170
FT SEQUENCE 262 AA; 28968 MW; DA87363A0D92BAF4 CRC64;
SQ
Query Match 47.1%; Score 65; DB 1; Length 262;
Best Local Similarity 57.1%; Pred. No. 0.014;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
1 IVGGXEVTPHAYFWQVGLFID 21
29 IIGGNEVTPHSRPMVLLSLD 49

```

Search completed: May 30, 2003, 11:02:43  
Job time : 23 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 10:57:47 ; Search time 79 Seconds  
(without alignments)  
65.205 Million cell updates/sec

Title: US-09-549-642-20  
Perfect score: 138  
Sequence: 1 IGVGXEVTTPHAYPMQVGLFIDMYF 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
1 number of hits satisfying chosen parameters: 671580

Maximum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvrius.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	73.2	271	5	018487
2	95	68.8	270	5	08WR11
3	94	68.1	265	5	018488
4	89	64.5	270	5	Q27824
5	77	55.8	254	6	Q9XSN6
6	76	55.1	474	5	Q8T4N3
7	74	53.6	309	5	Q27083
8	72	52.2	255	11	Q9Z0M1
9	72	52.2	255	11	Q9JIS2
10	72	52.2	270	5	Q96871
11	71	51.4	465	5	Q9EJL7
12	69	50.0	467	5	Q967X8
13	69	50.0	868	5	Q9V1V3
14	69	50.0	1524	13	Q91674
15	67	48.6	263	13	Q9PMQ6
16	66	47.8	260	13	Q9W7Q3

17	66	47.8	269	11	Q9D7T9	Q9d7t9 mus musculus
18	66	47.8	269	11	Q9CQ52	Q9cq52 mus musculus
19	66	47.8	492	4	Q9ET73	Q9et73 homo sapien
20	65	47.1	20	13	Q9PRR4	Q9prrr4 scyllorhinu
21	65	47.1	249	11	Q9QYN4	Q9qyn4 mus musculus
22	65	47.1	276	11	Q9QYN3	Q9qyn3 mus musculus
23	64	46.4	20	13	Q9PRR3	Q9prrr3 scyllorhinu
24	64	46.4	244	13	Q8QGW3	Q8qgw3 anguilla ja
25	64	46.4	266	13	Q9W7Q0	Q9w7q0 paralichthy
26	64	46.4	276	5	P91894	P91894 arenicola m
27	63	45.7	233	4	Q96RZ7	Q96rz7 homo sapien
28	63	45.7	247	13	Q42158	Q42158 petromyzon
29	63	45.7	247	13	Q42608	Q42608 petromyzon
30	63	45.7	273	6	Q9XSM1	Q9xsm1 ovis aries
31	63	45.7	273	11	Q921N4	Q921n4 mus musculus
32	63	45.7	275	4	Q96RZ6	Q96rz6 homo sapien
33	63	45.7	745	13	Q9PVY3	Q9pvvy3 cyprinus ca
34	63	45.7	806	6	Q18783	Q18783 macropus eu
35	63	45.7	812	11	Q9R0W3	Q9r0w3 rattus norv
36	63	45.7	812	11	Q91WJ5	Q91wj5 mus musculus
37	62	44.9	159	4	Q96PT1	Q96pt1 homo sapien
38	62	44.9	195	4	Q96PT0	Q96pt0 homo sapien
39	62	44.9	244	13	Q42159	Q42159 petromyzon
40	62	44.9	245	5	Q9BLI8	Q9bli8 lumbricus r
41	62	44.9	245	13	Q42160	Q42160 petromyzon
42	62	44.9	246	5	Q9BLI7	Q9bli7 lumbricus r
43	62	44.9	282	5	Q25395	Q25395 lumbricus r
44	62	44.9	283	5	Q25394	Q25394 lumbricus r
45	62	44.9	283	5	Q95V22	Q95v22 lumbricus b

## ALIGNMENTS

### RESULT 1

018487	018487	PRELIMINARY;	PRT;	271 AA.
ID	018487			
AC	018487			
DC	01-JAN-1998 (TrEMBLrel. 05, Created)			
DT	01-JAN-1998 (TrEMBLrel. 05, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Chymotrypsin BI (Fragment).			
GN	CHYMOTRYPSIN A.			
OS	Penaeus vannamei (Penaeid shrimp) (European white shrimp).			
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;			
OC	Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;			
OC	Penaeidae; Litopenaeus.			
OX	NCBI_TaxID=6689;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=SPERMATOPHORUS;			
RX	MEDLINE=99337490; PubMed=10407165;			
RA	Sellos D.Y., Van Wormhoudt A.;			
RT	"Polymorphism and evolution of collagenolytic serine protease genes in crustaceans."			
RL	Biochim. Biophys. Acta 1432:419-424(1999).			
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.			
CC	EMBL; Y10664; CAA71672.1; -.			
DR	HSSP; P00771; IAZZ.			
DR	MEROPS; S01.122; -.			
DR	InterPro; IPR001314; Chymotrypsin.			
DR	InterPro; IPR001254; Ser.protease_Try.			
DR	Pfam; PF00089; trypsin; 1.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	SMART; SM00020; TRYP_SPC; 1.			
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.			
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.			
DR	PROSITE; PS00135; TRYPSIN_SER; 1.			
KW	Hydrolase; Serine protease.			
FT	NON_TER 271 271			
SQ	SEQUENCE 271 AA; 28743 MW; EAD3F41DD6053ADE CRC64;			

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Query Match 73.2%; Score 101; DB 5; Length 271;
Best Local Similarity 72.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
DB 46 IVGGVEATPHSWPHQALFIDDMYF 70

RESULT 2
Q8WR11 PRELIMINARY; PRT; 270 AA.
AC Q8WR11;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Collagenolytic serine protease.
OS Paraliithodes camtschatica (kamchatka crab) (Red king crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;
Lithodidae; Paraliithodes.
NCBI_TaxID=6741;
RN [1]
RP SEQUENCE FROM N.A.
RA Rudenskaya G.N.; Kisiltsin Y.A.; Rebrikov D.V.; Kuranova I.P.;
RT "King crab Paraliithodes camtschaticus Collagenolytic serine protease
PC and Trypsin PC: cDNA cloning, primary structure and molecular
RT modeling of the enzymes.";
RL J. Protein Chem. 0:0-0(2002).
DR EMBL: AF461035; AAL67441.1; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Protease.
SQ SEQUENCE 270 AA; 28157 MW; 0CD1F574C5C1BD52 CRC64;

Query Match 68.8%; Score 95; DB 5; Length 270;
Best Local Similarity 72.0%; Pred. No. 2.9e-06;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
DB 45 IVGGVEATPHWVHVALFIDDMYF 69

RESULT 3
Q18488 PRELIMINARY; PRT; 265 AA.
AC Q18488;
DT 01-JAN-1998 (TremBLrel. 05, Created)
DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)
DE 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Chymotrypsin BII precursor (Fragment).
GN CHYMOTRYPSIN B.
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
NCBI_TaxID=6689;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-SPERMATOPHORUS;
RX MEDLINE=99337490; PubMed=10407165;
RA Sello D.Y.; Van Wormhoudt A.;
RT "Polymorphism and evolution of collagenolytic serine protease genes in
RT crustaceans.";
RL Biochim. Biophys. Acta 1432:419-424(1999).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
```

```
TRYPSIN FAMILY.
CC EMBL: Y10665; CAA71673.1; -.
DR HSP; P00771; IAZZ.
DR MEROPS; S01.122; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Signal.
FT NON_TER 1 1
FT SIGNAL <1 8 POTENTIAL.
FT NON_TER 265 265
FT NON_TER 265 265
SQ SEQUENCE 265 AA; 27895 MW; E6F6FC216C2ECE63 CRC64;

Query Match 68.1%; Score 94; DB 5; Length 265;
Best Local Similarity 68.0%; Pred. No. 4e-06;
Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
DB 40 IVGGTEAVPHSWPHQVAFIDGMYF 64

RESULT 4
Q27824 PRELIMINARY; PRT; 270 AA.
ID Q27824;
AC Q27824;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Serine collagenase 1 precursor (EC 3.4.21.32).
OS Uca pugilator (Atlantic sand fiddler crab) (Celuca pugilator).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Ocypodidae; Ocypodidae; Ocypodidae; Uca complex; Celuca.
OX NCBI_TaxID=6772;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HEPATOPANCREAS;
RX MEDLINE=96212234; PubMed=8626718;
TSU C.A.; Craik C.S.;
RT "Substrate recognition by recombinant serine collagenase 1 from Uca
RT pugilator.";
RL J. Biol. Chem. 271:11563-11570(1996).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
CC EMBL: U49331; AAC47030.1; -.
DR HSP; P00771; IAZZ.
DR MEROPS; S01.122; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Collagen; Hydrolyase; Serine protease; Signal.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 45 270 SERINE COLLAGENASE 1.
SQ SEQUENCE 270 AA; 28170 MW; C084D974968ED687 CRC64;

Query Match 64.5%; Score 89; DB 5; Length 270;
Best Local Similarity 64.0%; Pred. No. 2.3e-05;
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
DB 45 IVGGVEAVPHSWPHQVAFIDDMYF 69
```

```
RESULT 5
Q9XSN6 PRELIMINARY; PRT; 254 AA.
AC Q9XSN6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Enamel matrix serine proteinase 1 precursor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98126310; PubMed=9465170;
RA Simmer J.P., Fukue M., Tanabe T., Yamakoshi Y., Uchida T., Xue J.,
RA Margolis H.C., Shimizu M., DeHart B.C., Hu C.-C., Bartlett J.D.;
RA "Purification, characterization, and cloning of enamel matrix serine
proteinase 1.";
J. Dent. Res. 77:377-386(1998).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
CC EMBL; U76256; AAB94638.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.251; -.
DR InterPro; IPR001314; Chymotrypsin.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 31 254 ENAMEL MATRIX SERINE PROTEINASE 1.
SQ SEQUENCE 254 AA; 27235 MW; FD40EF95664406F1 CRC64;

Query Match 55.8%; Score 77; DB 6; Length 254;
Best Local Similarity 44.0%; Pred. No. 0.0013;
Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPMQVGLFIDMYF 25
DB 31 IINGDCNPHSQPMQAAFLFLEDDFF 55

RESULT 6
Q8T4N3 PRELIMINARY; PRT; 474 AA.
AC Q8T4N3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Midgut serine proteinase-2.
OS Rhipicephalus appendiculatus (Brown ear tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.
OX NCBI_TaxID=34631;
RN [1]
RP SEQUENCE FROM N.A.
RX Mulenga A., Onuma M., Sugimoto C.;
RT "Rhipicephalus appendiculatus midgut serine proteinase-2, cDNA cloning
and characterization.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY078094; AAL79566.1; -.
SQ SEQUENCE 474 AA; 51232 MW; B01330E1F00EF49F CRC64;

Query Match 55.1%; Score 76; DB 5; Length 474;
Best Local Similarity 66.7%; Pred. No. 0.0036;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPMQVGLFIDMYF 25
DB 31 IINGDCNPHSQPMQAAFLFLEDDFF 55

RESULT 7
Q27083 PRELIMINARY; PRT; 309 AA.
AC Q27083;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Clotting factor G beta subunit precursor.
OS Tachypleus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypleus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94117453; PubMed=8288603;
RA Seki N., Muta T., Oda T., Iwaki D., Kuma K., Miyata T., Iwanaga S.;
RT "Horseshoe crab (1,3)-beta-D-glucan-sensitive coagulation factor G. A
serine protease zymogen heterodimer with similarities to beta-gluca-
binding proteins.";
J. Biol. Chem. 269:1370-1374(1994).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
CC EMBL; D16623; BAA04045.1; -.
DR HSSP; P20231; IAAO.
DR MEROPS; S01.222; -.
DR InterPro; IPR001314; Chymotrypsin.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 309 CLOTTING FACTOR G BETA SUBUNIT.
SQ SEQUENCE 309 AA; 34255 MW; 014F0B5F2BD56FDB CRC64;

Query Match 53.6%; Score 74; DB 5; Length 309;
Best Local Similarity 57.9%; Pred. No. 0.0046;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPMQVGLF 19
DB 47 IINGGIATPHSWPMVGVIF 65

RESULT 8
Q9Z0M1 PRELIMINARY; PRT; 255 AA.
AC Q9Z0M1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Enamel matrix serine proteinase 1 precursor.
GN K1K4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SWISS-WEBSTER;
RX MEDLINE=20152522; PubMed=10690663;
RA Hu J.C.-C., Ryu O.H., Chen J.J., Uchida T., Wakida K., Murakami C.,
RA Jiang H., Qian Q., Zhang C., Ottmers V., Bartlett J.D., Simmer J.P.;
RA "Localization of EMSPI expression during tooth formation and cloning
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DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 32 255 ENAMEL MATRIX SERINE PROTEINASE 1.
FT VARIANT 15 15 Y -> C.
FT VARIANT 251 251 T -> I.
SQ SEQUENCE 255 AA; 27536 MW; CBF5BFAF7D4D679C CRC64;

Query Match 52.2%; Score 72; DB 11; Length 255;
Best Local Similarity 44.0%; Pred. No. 0.0076;
Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Oy 1 IVGGKEVTPHAYPMQVGLFIDDMYF 25
    I : : : : : : : : : : : : : :
Db 32 IIQGDQSPHSQPMQQAALFSDGFF 56

RESULT 10
O96871 PRELIMINARY; PRT; 270 AA.
AC O96871.
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Serine proteinase.
OS Trichinella spiralis.
OC Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida;
OC Trichinellidae; Trichinella.
OX NCBI_TaxID=6334;
RN [1]
RP SEQUENCE FROM N.A.
RA Todorova V., Xia Y., Moore J., Kennedy M.W.;
RT spiralis.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL: U62659; AAD09211.1; -.
DR HSP; P00763; IDPO.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 270 AA; 28325 MW; 6E5233084FBB13B7 CRC64;

Query Match 52.2%; Score 72; DB 5; Length 270;
Best Local Similarity 60.0%; Pred. No. 0.008;
Matches 12; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Oy 1 IVGGKEVTPHAYPMQVGLFI 20
    I : : : : : : : : : : : :
Db 39 IVGGSDAVPHSYPMQQAHLI 58

RESULT 11
O9BJL7 PRELIMINARY; PRT; 465 AA.
AC O9BJL7.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Newborn larvae-specific serine protease SS2.
OS Trichinella spiralis.
OC Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida;
OC Trichinellidae; Trichinella.
OX NCBI_TaxID=6334;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=ISS 534;
RA Liu M., Li C., Garcia-Reyna P., Fu B., Roman T., Boireau P.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL: AF331160; AAK16520.1; -.
DR HSP; P00763; IDPO.
DR InterPro: IPR000875; Chymotrypsin.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS00268; CECROPIN; UNKNOWN_1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Hydrolase: Protease; Serine protease.
CC SEQUENCE 465 AA; 50594 MW; 28B60795C5DA3EB1 CRC64;

Query Match 51.43; Score 71; DB 5; Length 465;
Best Local Similarity 61.13; Pred. No. 0.02;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPMQVGL 18
Db 82 IVGGTDVRPHSHPWQIOL 99

RESULT 12
Q967X8 PRELIMINARY; PRT; 467 AA.
AC Q967X8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CUB-serine protease.
OS Panulirus argus (Spiny lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;
OC Palinuroidea; Palinuridae; Panuliridae; Panulirus.
OX NCBI_TaxID=6737;
RN SIGNAL 1
RP SEQUENCE FROM N.A.
RA Levine M.Z., Walthall W.W., Tai P.C., Derby C.D.;
RL "Molecular cloning, characterization, cellular localization and
possible function of a CUB-serine protease in the olfactory system of
the spiny lobster Panulirus argus.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF357226; AAK48894.1; -.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00089; trypsin; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase: Protease; Serine protease.
SQ SEQUENCE 467 AA; 50453 MW; 1D2E663D3314BBFD CRC64;

Query Match 50.08; Score 69; DB 5; Length 467;
Best Local Similarity 58.38; Pred. No. 0.039;
Matches 14; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPMQVGLFIDDMY 24
Db 229 IVGGQETEVEVNEYPWQVLLVTRDMY 252

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RESULT 13
Q9Y1V3 PRELIMINARY; PRT; 868 AA.
AC Q9Y1V3
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tunicate retinoic acid-inducible modular protease precursor.
GN TRAMP.
OS Polyandrocarpa misakiensis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Scolidobranchia; Styelidae; Polyandrocarpa.
OX NCBI_TaxID=7723;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE SPOT;
RX MEDLINE=99423646; PubMed=10491255;
RA Ohashi M., Kawamura K., Fujii N., Yubisui T., Fujiwara S.;
RT "A retinoic acid-inducible modular protease in budding ascidians.";
RL Dev. Biol. 214:38-45(1999).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL: AB030007; BAA82522.1; -.
DR HSP; P00763; IDPO.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR002172; LDL_recept_A.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR001190; Srcr_receptor.
DR Pfam: PF00057; ldl_recept_a; 3.
DR Pfam: PF00530; SRCR; 2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00261; LDLRECEPTOR.
DR PRINTS: PR00258; SPERACTRCPTR.
DR SMART: SM00192; LDLa; 3.
DR SMART: SM00473; PAN_AP; 1.
DR SMART: SM00020; SR; 2.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS01209; LDLRA_1; 3.
DR PROSITE: PS00668; LDLRA_2; 3.
DR PROSITE: PS0287; SRCR_2; 2.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL 1
SQ SEQUENCE 868 AA; 97660 MW; F71452865F36A6CA CRC64;

Query Match 50.08; Score 69; DB 5; Length 868;
Best Local Similarity 44.08; Pred. No. 0.074;
Matches 11; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25
Db 624 IVGGSGTEPHEWPWQAGIWLPTWY 648

RESULT 14
Q91674 PRELIMINARY; PRT; 1524 AA.
AC Q91674
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Polyprotein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE-99432219; PubMed-10500163;
RA Lindsay L.L., Yang J.C., Hedrick J.L.;
RT "Ovocytase, a Xenopus laevis egg extracellular protease, is
RT translated as part of an unusual polypeptide."
RL Proc. Natl. Acad. Sci. U.S.A. 96:11253-11258(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Yang J.C., Lindsay L.L., Hedrick J.L.;
RT "cDNA Cloning of Ovocytase, a Chymotrypsin-like Protease Released
RT From Xenopus laevis Eggs at Fertilization."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 4 CUB DOMAINS.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; U81290; AAC24717.1; -.
DR HSSP; P00763; 1DPO.
DR MEROPS; S01.022; -.
DR MEROPS; S01.245; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000859; CUB_domain.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00089; trypsin; 3.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00042; CUB; 4.
DR SMART; SM00020; Tryp_Spc; 3.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS02040; TRYPSIN_DOM; 3.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_3.
DR PROSITE; PS00135; TRYPSIN_SER; 3.
KW Hydrolyase; Serine protease.
FT CHAIN 57 308 SERINE PROTEASE.
FT CHAIN 584 817 SERINE PROTEASE.
FT CHAIN 1295 1524 OVOCHYMASE.
SQ SEQUENCE 1524 AA; 167566 MW; 32EFE42128F37268 CRC64;

Query Match 50.0%; Score 69; DB 13; Length 1524;
Best Local Similarity 57.9%; Pred. No. 0.13;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Oy 1 IVGGXVTPHAYPWQVGLF 19
Db 584 IVGGEASPSNWPQVQIF 602

RESULT 15
O9PWQ6 PRELIMINARY; PRT; 263 AA.
O9PWQ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Chymotrypsin B precursor (EC 3.4.21.1).
GN CHVB.
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PYLORIC CAECA;
RX MEDLINE-20464334; PubMed-11011764;
RA Spilliaert R., Gudmundsdottir A.;
RT "Molecular Cloning of the Atlantic Cod Chymotrypsinogen B.";
RL Microb. Comp. Genomics 5:41-50(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AJ242521; CAB843766.1; -.
DR HSSP; P00766; 1CHG.
DR MEROPS; S01.152; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_Try.
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DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 263 CHYMOTRYPSIN B.
SQ SEQUENCE 263 AA; 28175 MW; EF61B18A34EE5E7C CRC64;

Query Match 48.6%; Score 67; DB 13; Length 263;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 IVGGXVTPHAYPWQVGL 18
Db 32 IVNGEAVPHSWPQVSL 49

Search completed: May 30, 2003, 11:04:09
Job time : 80 secs
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